

CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
 CC polynucleotides are useful as probes and primers for the amplification or
 CC detection of 121P1F1 genes, as coding sequences for directing the
 CC expression of 121P1F1 polypeptides, or as tools for modulating or
 CC inhibiting the expression of 121P1F1 genes. The present sequence is used
 CC in the exemplification of the present invention.

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.8e-88;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGSAEKKRTRMEIFSETQVFLKDLKIAPEKIGITMSYKEVLQSLVDGMV 60

Db 1 MSKKKGSAEKKRTRMEIFSETQVFLKDLKIAPEKIGITMSYKEVLQSLVDGMV 60

Qy 61 DCEKIGTSNYMAPPSPKALHARKHKLKLEVLSESGSKHSLQKSIKAKIGRCETEE 120

Db 61 DCEKIGTSNYMAPPSPKALHARKHKLKLEVLSESGSKHSLQKSIKAKIGRCETEE 120

Qy 121 TRLAKESSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKYAKKAAANRMTDNIFAISWA 180

Db 121 TRLAKESSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKYAKKAAANRMTDNIFAISWA 180

Qy 181 KRKGFEBENKIDRTFGIPEDFDYID 205

Db 181 KRKGFEBENKIDRTFGIPEDFDYID 205

RESULT 2

ADJ70015

ID ADJ70015 standard; protein; 205 AA.

XX ADJ70015;

Qy 06-MAY-2004 (first entry)

Db Human heat mitochondrial protein as a therapeutic target SegID1821.

XX mitochondrial; human; screening assay; diabetes mellitus;

KM Huntington's disease; osteoarthritis;

KM Leber's hereditary optic neuropathy; LHON;

KM mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KM myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KM neuroprotective; noctropic; antidiabetic; anticonvulsant; antiarthritic;

KM osteopathic; ophthalmological; cytostatic.

XX Homo sapiens.

OS WO2003087768-A2.

XX 23-OCT-2003.

PD 04-APR-2003; 2003WO-US010870.

XX 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987P.

PR 20-SEP-2002; 2002US-0412418P.

XX (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW,

PI Warmock DE;

XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for

PT treating diseases associated with altered mitochondrial function,

PT comprises detecting a modified polypeptide in a sample and correlating

PT with the disease.

PS Claim 1; SEQ ID NO 1821; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used

CC for therapeutic intervention in treating a disease associated with

CC altered mitochondrial function. Specifically, it refers to a method for

CC identifying proteins of the human heart mitochondrial proteome that are

CC useful for drug screening assays, as well as therapeutic targets. The

CC present invention describes a method for identifying such proteins that

CC can be used in the treatment of various diseases associated with altered

CC mitochondrial function including diabetes mellitus, Huntington's disease,

CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy

CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

CC compositions have neuroprotective, noctropic, antidiabetic,

CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytostatic activities. This polypeptide sequence is a human heart

XX mitochondrial protein of the invention.

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 7; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.8e-88;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGSAEKKRTRMEIFSETQVFLKDLKIAPEKIGITMSYKEVLQSLVDGMV 60

Db 1 MSKKKGSAEKKRTRMEIFSETQVFLKDLKIAPEKIGITMSYKEVLQSLVDGMV 60

Qy 61 DCEKIGTSNYMAPPSPKALHARKHKLKLEVLSESGSKHSLQKSIKAKIGRCETEE 120

Db 61 DCEKIGTSNYMAPPSPKALHARKHKLKLEVLSESGSKHSLQKSIKAKIGRCETEE 120

Qy 121 TRLAKESSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKYAKKAAANRMTDNIFAISWA 180

Db 121 TRLAKESSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKYAKKAAANRMTDNIFAISWA 180

Qy 181 KRKGFEBENKIDRTFGIPEDFDYID 205

Db 181 KRKGFEBENKIDRTFGIPEDFDYID 205

RESULT 3

ADM83851

ID ADM83851 standard; protein; 205 AA.

XX ADM83851;

Qy 03-JUN-2004 (first entry)

Db Human cancer gene 121P1F1 protein #6.

XX Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;

KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;

KM colon cancer; lung cancer; pancreatic cancer; breast cancer;

KM cervical cancer; stomach cancer; gene therapy; vaccine.

XX Homo sapiens.

OS US2003223997-A1.

XX 04-DEC-2003.

XX Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX WPI: 2004-060522/06.
XX
XX New composition comprising a substance that modulates the status of
PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
XX Example 5; SEQ ID NO 61; 211pp; English.
XX
XX The invention relates to a composition comprising a substance that
CC modulates the status of 121PI1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121PI1 where status of the cell
CC that expresses 121PI1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121PI1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121PI1, inhibiting growth of cancer cells that expresses
CC 121PI1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121PI1, generating a
CC mammalian immune response directed to 121PI1, inducing an immune
CC response, monitoring 121PI1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121PI1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121PI1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121PI1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121PI1. The gene for 121PI1 is located on chromosome 4q. The present
CC sequence is a 121PI1 protein (full-length or fragment).
XX
XX Sequence 205 AA;
SQ
Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGSAEERKPTMEIFSETKOVFOKLEKIAPEKGTITANSVEKLSLVDDGMV 60
DB 1 MSKKKGSAEERKPTMEIFSETKOVFOKLEKIAPEKGTITANSVEKLSLVDDGMV 60
QY DCEIRGTSNYWAFPSKALHARKHLEVLSEQLSEGSOKHASLOKSEIKAKIGRCETEER 120
DB DCEIRGTSNYWAFPSKALHARKHLEVLSEQLSEGSOKHASLOKSEIKAKIGRCETEER 120
QY 121 TRLAKELSLDQREQLKAEVETKDCDPQVEEIRQANKYAKAANRWNTNIFAIKSWA 180
DB 121 TRLAKELSLDQREQLKAEVETKDCDPQVEEIRQANKYAKAANRWNTNIFAIKSWA 180
QY 181 KRKGFEEENKIDRTGPIEDPEYID 205
DB 181 KRKGFEEENKIDRTGPIEDPEYID 205
RESULT 4

ADM83810
ID ADM83810 standard; protein; 205 AA.
XX
XX ADM83810;
AC
XX 03-JUN-2004 (first entry)
DT
XX Human cancer gene 121PI1 protein #3.
DE
XX Human; cancer gene 121PI1; cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
KW cervical cancer; stomach cancer; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX US200323997-A1.
PN
XX 04-DEC-2003.
PD
XX 28-FEB-2002; 2002US-00087190.
PF
XX 08-FEB-2001; 2001US-00779250.
PR
XX (CHAL/) CHAILITA-EID P M.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARIS/) FARIS M.
PA (AFAR/) AFAR D E H.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
XX WPI: 2004-060522/06.
XX
XX New composition comprising a substance that modulates the status of
PT 121PI1 or a molecule that is modulated by 121PI1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
XX Disclosure; SEQ ID NO 20; 211pp; English.
XX
XX The invention relates to a composition comprising a substance that
CC modulates the status of 121PI1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121PI1 where status of the cell
CC that expresses 121PI1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121PI1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121PI1, inhibiting growth of cancer cells that expresses
CC 121PI1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121PI1, generating a
CC mammalian immune response directed to 121PI1, inducing an immune
CC response, monitoring 121PI1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121PI1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121PI1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121PI1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121PI1 or its
CC splice variants. The composition is useful for detecting, treating or

CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 205 AA;
Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60
Db 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60
QY 61 DCEKIGTNTYMAFPSPKALHARKHKLVLBSQLSBGSQKASLQKSTKAKIGCEETEE 120
Db 61 DCEKIGTNTYMAFPSPKALHARKHKLVLBSQLSBGSQKASLQKSTKAKIGCEETEE 120
QY 121 TRLAKELSLRDQREOLKAVEKYKCDPQVVEIRQANKYAKKAARMTDNIPIKSWA 180
Db 121 TRLAKELSLRDQREOLKAVEKYKCDPQVVEIRQANKYAKKAARMTDNIPIKSWA 180
QY 181 KRKGFPEENKIDRTFGIPEDFDYID 205
Db 181 KRKGFPEENKIDRTFGIPEDFDYID 205
RESULT 5
ADM83812
ID ADM83812 standard; protein; 205 AA.
XX
AC ADM83812;
XX 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1F1 protein #5.
XX
XX Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
KM cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2003223997-A1.
XX
PD 04-DEC-2003.
XX
PF 28-FEB-2002; 2002US-00087190.
XX
PR 08-FEB-2001; 2001US-00779250.
XX
PA (CHAL/) CHALLITA-EID P M.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARI/) PARIS M.
PA (AFAR/) AFAR D E H.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
DR WPI; 2004-060522/06.
XX
XX New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
XX lung cancer.
XX

PS Disclosure; SEQ ID NO 22; 211pp; English.
XX
XX The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 205 AA;
Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60
Db 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKIGITAMSYKVLQSLVDDGMV 60
QY 61 DCEKIGTNTYMAFPSPKALHARKHKLVLBSQLSBGSQKASLQKSTKAKIGCEETEE 120
Db 61 DCEKIGTNTYMAFPSPKALHARKHKLVLBSQLSBGSQKASLQKSTKAKIGCEETEE 120
QY 121 TRLAKELSLRDQREOLKAVEKYKCDPQVVEIRQANKYAKKAARMTDNIPIKSWA 180
Db 121 TRLAKELSLRDQREOLKAVEKYKCDPQVVEIRQANKYAKKAARMTDNIPIKSWA 180
QY 181 KRKGFPEENKIDRTFGIPEDFDYID 205
Db 181 KRKGFPEENKIDRTFGIPEDFDYID 205
RESULT 6
ADM83793
ID ADM83793 standard; protein; 205 AA.
XX
AC ADM83793;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human cancer gene 121P1F1 protein #1.
XX
XX Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KM

KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KM cervical cancer; stomach cancer; gene therapy; vaccine.
 XX Homo sapiens.
 XX US2003223997-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-FEB-2002; 2002US-00087190.
 PR 08-FEB-2001; 2001US-00779250.
 XX
 PA (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 XX
 XX WPI; 2004-060522/06.
 DR N-PSDB; ADM83792.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121PIPI or a molecule that is modulated by 121PIPI, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 PS
 XX Claim 19; SEQ ID NO 3; 211pp; English.
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121PIPI (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121PIPI where status of the cell
 CC that expresses 121PIPI is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody
 CC that immunospecifically binds to a 121PIPI-related protein (comprising
 CC the variable domains of the heavy and light chains of a monoclonal
 CC antibody), a vector comprising a polynucleotide that encodes a single
 CC chain monoclonal antibody, a polynucleotide that encodes an analogue
 CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
 CC that expresses 121PIPI, inhibiting growth of cancer cells that expresses
 CC 121PIPI (comprising administering to the cells the composition), treating
 CC a patient who bears cancer cells that express 121PIPI, generating a
 CC mammalian immune response directed to 121PIPI, inducing an immune
 CC response, monitoring 121PIPI gene products in a biological sample from a
 CC patient who has or who is suspected of having cancer, monitoring the
 CC presence of cancer in an individual and an assay for detecting the
 CC presence of a 121PIPI-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC composition may comprise a polynucleotide that comprises a 121PIPI-
 CC related protein coding sequence provided that the coding sequence does
 CC not encode the entire amino acid sequence of 121PIPI (ADM83793). The
 CC substance also comprises a polynucleotide that encodes at least one
 CC peptide given in 16 Tables (given in the specification), the peptides
 CC being HLA (human leukocyte antigen)-binding epitopes from 121PIPI or its
 CC splice variants. The composition is useful for detecting, treating or
 CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
 CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
 CC cervical cancer or stomach cancer. The composition can also be used as a
 CC vaccine to treat or prevent cancer that expresses or overexpresses
 CC 121PIPI. The gene for 121PIPI is located on chromosome 4q. The present
 CC sequence is a 121PIPI protein (full-length or fragment).
 XX
 XX Sequence 205 AA;
 SQ
 Query Match 100.0%; Score 1047; DB 8; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.8e-88;
 Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSKKKGLSAEKKRTMWEI FSETKDV FOLKLEKIA PKKGI TAMS VKEVLQSLVDGMY 60
 DB 1 MSKKKGLSAEKKRTMWEI FSETKDV FOLKLEKIA PKKGI TAMS VKEVLQSLVDGMY 60
 QY 61 DCEKIGTSNYWYAPPSKALHARKHLEVLSEQLSGSQKHASLQKSI EKAKI GRCETERR 120
 DB 61 DCEKIGTSNYWYAPPSKALHARKHLEVLSEQLSGSQKHASLQKSI EKAKI GRCETERR 120
 QY 121 TRLAKEISLDRQREQLAEVEKYKDCDPVVEEIRQANKYAKKANRWTDNI FAIKSMA 180
 DB 121 TRLAKEISLDRQREQLAEVEKYKDCDPVVEEIRQANKYAKKANRWTDNI FAIKSMA 180
 QY 181 KRKFGFEENKIDRTGPIPEDFDYID 205
 DB 181 KRKFGFEENKIDRTGPIPEDFDYID 205
 RESULT 7
 ID ADM83811 standard; protein; 205 AA.
 XX
 XX ADM83811;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human cancer gene 121PIPI protein #4.
 XX
 XX Human; cancer gene 121PIPI; cytostatic; cancer; chromosome 4q; HLA;
 KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
 KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
 KW cervical cancer; stomach cancer; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX US2003223997-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-FEB-2002; 2002US-00087190.
 PR 08-FEB-2001; 2001US-00779250.
 XX
 PA (CHAL/) CHALLITA-EID P M.
 PA (HUBE/) HUBERT R S.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (AFAR/) AFAR D E H.
 PA (GEW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
 PI Jakobovits A;
 XX
 XX WPI; 2004-060522/06.
 DR
 PT New composition comprising a substance that modulates the status of
 PT 121PIPI or a molecule that is modulated by 121PIPI, useful for detecting,
 PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
 PT lung cancer.
 PS
 XX Disclosure; SEQ ID NO 21; 211pp; English.
 CC The invention relates to a composition comprising a substance that
 CC modulates the status of 121PIPI (a protein encoded by a cancer expressed
 CC gene) or a molecule that is modulated by 121PIPI where status of the cell
 CC that expresses 121PIPI is modulated. Also included are a pharmaceutical
 CC composition comprising the novel composition in a human unit dose form, a
 CC recombinant protein comprising an antigen-binding region of a monoclonal
 CC antibody, a non-human transgenic animal that produces an antibody, a
 CC hybridoma that produces an antibody, a single chain monoclonal antibody

CC that immunospecifically binds to a 121PIPI-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121PIPI, inhibiting growth of cancer cells that expresses
CC 121PIPI (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121PIPI, generating a
CC mammalian immune response directed to 121PIPI, inducing an immune
CC response, monitoring 121PIPI gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121PIPI-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121PIPI-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121PIPI (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121PIPI or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121PIPI. The gene for 121PIPI is located on chromosome 4q. The present
CC sequence is a 121PIPI protein (full-length or fragment).

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRRRMETFSSETDVPQLKLEKIAPEKIGITMSVKEVLSIVDDGMV 60
DB 1 MSKKKGSAEKKRRRMETFSSETDVPQLKLEKIAPEKIGITMSVKEVLSIVDDGMV 60
QY 61 DCEKIGTSNYWAFPSKALHARKHKLFLVLESQLSGSGOKHASLQKSIKAKIGCETTER 120
DB 61 DCEKIGTSNYWAFPSKALHARKHKLFLVLESQLSGSGOKHASLQKSIKAKIGCETTER 120
QY 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEVEIRQANKYAKKXANRWNTNIPAKSMA 180
DB 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEVEIRQANKYAKKXANRWNTNIPAKSMA 180
QY 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEVEIRQANKYAKKXANRWNTNIPAKSMA 180
DB 121 TRLAKELSLRDQREQLKAEVEKYKDCDPQVEVEIRQANKYAKKXANRWNTNIPAKSMA 180
QY 181 KRKGFENKIDRTFGIPEDPDYID 205
DB 181 KRKGFENKIDRTFGIPEDPDYID 205

RESULT 8

ADM83804
ID ADM83804 standard; protein; 205 AA.

AC ADM83804;

DT 03-JUN-2004 (first entry)

XX Human cancer gene 121PIPI protein #2.

XX Human; cancer gene 121PIPI; cytostatic; cancer; chromosome 4q; HLA;

KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;

KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
cervical cancer; stomach cancer; gene therapy; vaccine.

XX Homo sapiens.

OS US200323997-A1.

PN 04-DEC-2003.

PD 28-FEB-2002; 2002US-00087190.

XX 08-FEB-2001; 2001US-00779250.

PR (CHAL/) CHALILTA-ELID P M.

PA (HUBER/) HUBERT R S.

PA (RAIT/) RAITANO A B.

PA (FARIT/) FARIS M.

PA (AFAR/) AFAR D E H.

PA (GEMW/) GE W.

PA (JAKO/) JAKOBOVITS A.

XX Chailita-Elid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;

PI Jakobovits A;

XX WPI; 2004-060522/06.

DR New composition comprising a substance that modulates the status of

XX 121PIPI or a molecule that is modulated by 121PIPI, useful for detecting,

PT treating or preventing cancer e.g. prostate, bladder, colon, breast or

PT lung cancer.

XX Disclosure; SEQ ID NO 14; 211pp; English.

XX The invention relates to a composition comprising a substance that

XX modulates the status of 121PIPI (a protein encoded by a cancer expressed

XX gene) or a molecule that is modulated by 121PIPI where status of the cell

XX that expresses 121PIPI is modulated. Also included are a pharmaceutical

XX composition comprising the novel composition in a human unit dose form, a

XX recombinant protein comprising an antigen-binding region of a monoclonal

XX antibody, a non-human transgenic animal that produces an antibody, a

XX hybridoma that produces an antibody, a single chain monoclonal antibody

XX that immunospecifically binds to a 121PIPI-related protein (comprising

XX the variable domains of the heavy and light chains of a monoclonal

XX antibody), a vector comprising a polynucleotide that encodes a single

XX chain monoclonal antibody, a polynucleotide that encodes an analogue

XX peptide, delivering a cytotoxic agent or a diagnostic agent to a cell

XX that expresses 121PIPI, inhibiting growth of cancer cells that expresses

XX 121PIPI (comprising administering to the cells the composition), treating

XX a patient who bears cancer cells that express 121PIPI, generating a

XX mammalian immune response directed to 121PIPI, inducing an immune

XX response, monitoring 121PIPI gene products in a biological sample from a

XX patient who has or who is suspected of having cancer, monitoring the

XX presence of cancer in an individual and an assay for detecting the

XX presence of a 121PIPI-related protein or polynucleotide in a biological

XX sample from a patient who has or who is suspected of having cancer. The

XX composition may comprise a polynucleotide that comprises a 121PIPI-
related protein coding sequence provided that the coding sequence does
not encode the entire amino acid sequence of 121PIPI (ADM83793). The
substance also comprises a polynucleotide that encodes at least one
peptide given in 16 Tables (given in the specification), the peptides
being HLA (human leukocyte antigen)-binding epitopes from 121PIPI or its
splice variants. The composition is useful for detecting, treating or
preventing cancer, preferably prostate cancer, bladder cancer, kidney
cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
cervical cancer or stomach cancer. The composition can also be used as a
vaccine to treat or prevent cancer that expresses or overexpresses
121PIPI. The gene for 121PIPI is located on chromosome 4q. The present
sequence is a 121PIPI protein (full-length or fragment).

XX Sequence 205 AA;

Query Match 100.0%; Score 1047; DB 8; Length 205;
Best Local Similarity 100.0%; Pred. No. 1.8e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRRRMETFSSETDVPQLKLEKIAPEKIGITMSVKEVLSIVDDGMV 60
DB 1 MSKKKGSAEKKRRRMETFSSETDVPQLKLEKIAPEKIGITMSVKEVLSIVDDGMV 60
QY 61 DCEKIGTSNYWAFPSKALHARKHKLFLVLESQLSGSGOKHASLQKSIKAKIGCETTER 120
DB 61 DCEKIGTSNYWAFPSKALHARKHKLFLVLESQLSGSGOKHASLQKSIKAKIGCETTER 120

QY 121 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSMA 180
DB 121 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSMA 180
QY 181 KRKFGFEENKIDRTFGIPEDPDYID 205
DB 181 KRKFGFEENKIDRTFGIPEDPDYID 205

RESULT 9
ABP75541
ID ABP75541 standard; protein, 219 AA.
XX
AC ABP75541;
XX
DT 10-FEB-2003 (first entry)
XX
DE Human secretory polypeptide SPTM SEQ ID NO 725.
XX
KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;
KW anti-inflammatory; immunosuppressive; neuroprotective; neurotropic;
KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
KW antipsychotic; antianaemic; anti-HIV; human immunodeficiency virus;
KW secretory polynucleotide; secretory protein.
XX
OS Homo sapiens.
XX
PN MO200283876-A2.
XX
PD 24-OCT-2002.
XX
PF 27-MAR-2002; 2002MO-US0009921.
XX
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J,
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PG, Ameshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B,
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
XX WPI: 2003-075543/07.
DR N-PSDB; ABZ35987.
XX
XX New human secretory proteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
PT cancers.
XX
PS Claim 27; SEQ ID NO 725; 458bp + Sequence listing; English.

The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence, a polynucleotide complementary to them or an RNA equivalent of them. The polypeptide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease,

CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). The present sequence is one of the SPTM
CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 219 AA;
XX
Query Match 100.0%; Score 1047; DB 6; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.9e-88;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSLAEKRRRMEIFSETDVPOLKLEKAPKRGITMSVENVQSLVDDGV 60
DB 15 MSKKKGSLAEKRRRMEIFSETDVPOLKLEKAPKRGITMSVENVQSLVDDGV 74
QY 61 DCERIGTSNYWAPPSPKALHARKHLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 75 DCERIGTSNYWAPPSPKALHARKHLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 134
QY 121 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSMA 180
DB 135 TRLAKELSSLDQREQLKAEVEKTKDCDPQVVEEIRQANKVAKKANWNTDNIFAIKSMA 194
QY 181 KRKFGFEENKIDRTFGIPEDPDYID 205
DB 195 KRKFGFEENKIDRTFGIPEDPDYID 219

RESULT 10
ADM83834
ID ADM83834 standard; protein, 206 AA.
XX
XX ADM83834;
XX
AC ADM83834;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1, variant protein #1.
XX
KW Human; cancer gene 121P1, cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
KW cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2003223997-A1.
XX
XX 04-DEC-2003.
XX
PD 28-FEB-2002; 2002US-00087190.
XX
PF 08-FEB-2001; 2001US-00779250.
XX
PA (CHAL/) CHALLITA-EID P M.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARI M.
PA (AFAR/) AFAR D E H.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-eid PM, Hubert RS, Raitano AB, Fari M, Afar DEH, Ge W,
PI Jakobovits A;
XX
DR WPI: 2004-060522/06.
XX
XX New composition comprising a substance that modulates the status of

PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.

XX Example 5; SEQ ID NO 44; 211pp; English.

CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).

XX Sequence 206 AA;

Query Match 99.0%; Score 1036.5; DB 8; Length 206;
Best Local Similarity 99.5%; Pred. No. 1.7e-87;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKKGLSAEKKRTWMEIFSETKDVFLQKLEKTAPEKGIITAMSVKEVQLSLVDGMV 60
DB 1 MSKKKGLSAEKKRTWMEIFSETKDVFLQKLEKTAPEKGIITAMSVKEVQLSLVDGMV 60
QY 61 DCEKRGTSNYWAFPSKALHARKHLEVLSESGQSKASLOKSTIEKKGICETEE 119
DB 61 DCEKRGTSNYWAFPSKALHARKHLEVLSESGQSKASLOKSTIEKKGICETEE 120
QY 120 RTRIAKEKLSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRMTDNIFAISW 179
DB 121 RTRIAKEKLSLRDQEQKAEVEKYKDCDPVVEEIRQANKVAKAANRMTDNIFAISW 180
QY 180 AKRRKGFENKIDRTFGIPEDFDYID 205
DB 181 AKRRKGFENKIDRTFGIPEDFDYID 206

RESULT 11

ADM83835 ADM83835 standard; protein; 206 AA.

XX AC ADM83835;

DT 03-JUN-2004 (first entry)

XX

DE Human cancer gene 121P1F1 variant protein #2.

XX Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
KW cervical cancer; stomach cancer; gene therapy; vaccine.

XX Homo sapiens.

PN US2003223997-A1.

XX 04-DEC-2003.

XX 28-FEB-2002; 2002US-00087190.

XX 08-FEB-2001; 2001US-00779250.

PA (CHAL/) CHALILTA-EID P M.

PA (HUBE/) HUBERT R S.

PA (RAIT/) RAITANO A B.

PA (FARI/) FARIS M.

PA (AFAR/) AFAR D E H.

PA (GEW/) GE W.

PA (JAKO/) JAKOBOVITS A.

XX Chalilta-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,

XX Jakobovits A;

XX WPI; 2004-060522/06.

PT New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.

XX Example 5; SEQ ID NO 45; 211pp; English.

CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).

Seq Sequence 206 AA;

Query Match 99.0%; Score 1036.5; DB 8; Length 206;
Best Local Similarity 99.5%; Pred. No. 1.7e-87;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSKKGLSAEERKRTMMEIFSETKQVFOUKDLEKIAPKKEKGTITAMSVKEVLSLVDDGAV 60
DB 1 MSKKGLSAEERKRTMMEIFSETKQVFOUKDLEKIAPKKEKGTITAMSVKEVLSLVDDGAV 60
QY 61 DCEKGTSTNYWAFPSKALHARKHKLKLEVESQELSEGSGHSLQKSIERAKIGRCETEE 119
DB 61 DCEKGTSTNYWAFPSKALHARKHKLKLEVESQELSEGSGHSLQKSIERAKIGRCETEE 120
QY 120 RTFLAKELSLRDQREQLKAEVEKDYCDPQVVEIRQANKYAKKAAKNTDNIPIAKSM 179
DB 121 RTFLAKELSLRDQREQLKAEVEKDYCDPQVVEIRQANKYAKKAAKNTDNIPIAKSM 180
QY 180 AKRKFGEENKIDRTFGIPEDFDYID 205
DB 181 AKRKFGEENKIDRTFGIPEDFDYID 206

RESULT 12
ADM83814
ID ADM83814 standard; protein; 198 AA.
XX
AC ADM83814;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1F1 protein fragment.
XX
KM Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
KM human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KM colon cancer; lung cancer; pancreatic cancer; breast cancer;
KM cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
FN US2003223997-A1.
XX
PD 04-DEC-2003.
XX
PF 28-FEB-2002; 2002US-00087190.
XX
PR 08-FEB-2001; 2001US-00779250.
XX
PA (CHAL/) CHALLITA-EID P M.
XX
PA (HUBE/) HUBERT R S.
PA (RAT/) RATTANO A B.
PA (FARI/) PARIS M.
PA (AFAR/) AFAR D E H.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challaite-Bid PM, Hubert RS, Raicano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
DR WPI; 2004-060522/06.
XX
PT New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
PS Example 2; SEQ ID NO 24; 211pp; English.
XX
CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a

CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domains of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides
CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX

Seq Sequence 198 AA;

Query Match 96.6%; Score 1011; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.6e-85;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KGLSAEERKRTMMEIFSETKQVFOUKDLEKIAPKKEKGTITAMSVKEVLSLVDDGAVDCER 64
DB 1 KGLSAEERKRTMMEIFSETKQVFOUKDLEKIAPKKEKGTITAMSVKEVLSLVDDGAVDCER 60
QY 65 IGTSNYWAFPSKALHARKHKLKLEVESQELSEGSGHSLQKSIERAKIGRCETERTRIA 124
DB 61 IGTSNYWAFPSKALHARKHKLKLEVESQELSEGSGHSLQKSIERAKIGRCETERTRIA 120
QY 125 KELSLRDQREQLKAEVEKDYCDPQVVEIRQANKYAKKAAKNTDNIPIAKSMARKRF 184
DB 121 KELSLRDQREQLKAEVEKDYCDPQVVEIRQANKYAKKAAKNTDNIPIAKSMARKRF 180
QY 185 GFENKIDRTFGIPEDFD 202
DB 181 GFENKIDRTFGIPEDFD 198

RESULT 13
AAM40043
ID AAM40043 standard; protein; 190 AA.
XX
AC AAM40043;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 3188.
XX
KM Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KM peripheral nervous system; neuropathy; central nervous system; CNS;
KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KM leukaemia.
XX
OS Homo sapiens.
XX

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PN WO20015312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00468725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA,
XX Zhou P, Goodrich R, Dimanac RT;
XX
XX WPI; 2001-442253/47.
XX N-PSDB; AAI59199.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 3188; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57799-AAI61369) and the
XX encoded polypeptides (AAM36642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX Sequence 190 AA;
SQ
Query Match 93.1%; Score 975; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MMEIFSETKDVFOQLDKLEKIPKKEGKITAMSVKVLQSLVDGMDVCERIGTSNYMAFP 75
DB 1 MMEIFSETKDVFOQLDKLEKIPKKEGKITAMSVKVLQSLVDGMDVCERIGTSNYMAFP 60
QY 76 SKALHARKHKLKLEVLSEQSSEGSQGHASLQKSIIEKAKIGRCETBERTRLAKELSLRDQRE 135
DB 61 SKALHARKHKLKLEVLSEQSSEGSQGHASLQKSIIEKAKIGRCETBERTRLAKELSLRDQRE 120
QY 136 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 195
DB 121 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 180
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190

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RESULT 14
ADD84547
ID ADD84547 standard; protein; 190 AA.
XX

```

AC ADD84547;
XX
XX 29-JAN-2004 (first entry)
XX
XX 121PIPL1 variant 4 protein.
XX
XX 121PIPL1; 121PIPL1 modulation; human; chromosome 4q; cytostatic;
XX gene therapy; vaccine; cancer; immune response; immunisation.
XX
XX Synthetic.
XX OS Homo sapiens.
XX MO200295009-A2.
XX
XX 28-NOV-2002.
XX
XX 28-FEB-2002; 2002WO-US006242.
XX
XX 05-MAR-2001; 2001US-00799250.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
XX Jakobovits A;
XX
XX WPI; 2003-156757/15.
XX N-PSDB; ADD84546.
XX
XX Composition comprising a substance that modulates the status of 121PIPL1,
XX useful in diagnosing, preventing, prognosticating or treating patients
XX with cancer that expresses 121PIPL1, such as breast, colon, ovarian or
XX lung cancer.
XX
XX Claim 19; Fig 2F; 285pp; English.
XX
XX The present invention describes a composition (I) comprising a substance
XX that modulates the status of 121PIPL1 (gene and encoded protein), or a
XX molecule that is modulated by 121PIPL1, where the status of a cell that
XX expresses 121PIPL1 is modulated. The human 121PIPL1 gene maps to chromosome
XX 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
XX vaccines. The composition (I) can be used for diagnosing, preventing,
XX prognosticating or treating patients with cancer that expresses 121PIPL1,
XX such as breast, colon, ovarian or lung cancer. The 121PIPL1 gene or its
XX fragment can be used to elicit a humoral or cellular immune response.
XX 121PIPL1 antibodies can be used in active or passive immunisation. 121PIPL1
XX polynucleotides are useful as probes and primers for the amplification or
XX detection of 121PIPL1 genes, as coding sequences for directing the
XX expression of 121PIPL1 polypeptides, or as tools for modulating or
XX inhibiting the expression of 121PIPL1 genes. The present sequence is used
XX in the exemplification of the present invention.
XX
XX Sequence 190 AA;
SQ
Query Match 93.1%; Score 975; DB 7; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MMEIFSETKDVFOQLDKLEKIPKKEGKITAMSVKVLQSLVDGMDVCERIGTSNYMAFP 75
DB 1 MMEIFSETKDVFOQLDKLEKIPKKEGKITAMSVKVLQSLVDGMDVCERIGTSNYMAFP 60
QY 76 SKALHARKHKLKLEVLSEQSSEGSQGHASLQKSIIEKAKIGRCETBERTRLAKELSLRDQRE 135
DB 61 SKALHARKHKLKLEVLSEQSSEGSQGHASLQKSIIEKAKIGRCETBERTRLAKELSLRDQRE 120
QY 136 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 195
DB 121 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIFAIKSWAKRRKGFENKIDRTF 180
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190

```

RESULT 15
ADM83857
ID ADM83857 standard; protein; 190 AA.
XX
AC ADM83857;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human cancer gene 121P1F1 protein 16-205.
XX
KW Human; cancer gene 121P1F1, cytostatic; cancer; chromosome 4q; HLA;
KW human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
KW colon cancer; lung cancer; pancreatic cancer; breast cancer;
KW cervical cancer; stomach cancer; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN US2003223997-A1.
XX
PD 04-DEC-2003.
XX
PF 28-FEB-2002; 2002US-00087190.
PR 08-FEB-2001; 2001US-00779250.
XX
PA (CHAL/) CHALLITA-EID P M.
PA (HUBE/) HUBERT R S.
PA (RAIT/) RAITANO A B.
PA (FARIT/) FARIS M.
PA (AFAR/) AFAR D E H.
PA (GEW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
DR WPI; 2004-060522/06.
XX
PT New composition comprising a substance that modulates the status of
PT 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,
PT treating or preventing cancer e.g. prostate, bladder, colon, breast or
PT lung cancer.
XX
PS Example 5; SEQ ID NO 67; 211pp; English.
XX
CC The invention relates to a composition comprising a substance that
CC modulates the status of 121P1F1 (a protein encoded by a cancer expressed
CC gene) or a molecule that is modulated by 121P1F1 where status of the cell
CC that expresses 121P1F1 is modulated. Also included are a pharmaceutical
CC composition comprising the novel composition in a human unit dose form, a
CC recombinant protein comprising an antigen-binding region of a monoclonal
CC antibody, a non-human transgenic animal that produces an antibody, a
CC hybridoma that produces an antibody, a single chain monoclonal antibody
CC that immunospecifically binds to a 121P1F1-related protein (comprising
CC the variable domain of the heavy and light chains of a monoclonal
CC antibody), a vector comprising a polynucleotide that encodes a single
CC chain monoclonal antibody, a polynucleotide that encodes an analogue
CC peptide, delivering a cytotoxic agent or a diagnostic agent to a cell
CC that expresses 121P1F1, inhibiting growth of cancer cells that expresses
CC 121P1F1 (comprising administering to the cells the composition), treating
CC a patient who bears cancer cells that express 121P1F1, generating a
CC mammalian immune response directed to 121P1F1, inducing an immune
CC response, monitoring 121P1F1 gene products in a biological sample from a
CC patient who has or who is suspected of having cancer, monitoring the
CC presence of cancer in an individual and an assay for detecting the
CC presence of a 121P1F1-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC composition may comprise a polynucleotide that comprises a 121P1F1-
CC related protein coding sequence provided that the coding sequence does
CC not encode the entire amino acid sequence of 121P1F1 (ADM83793). The
CC substance also comprises a polynucleotide that encodes at least one
CC peptide given in 16 Tables (given in the specification), the peptides

CC being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or its
CC splice variants. The composition is useful for detecting, treating or
CC preventing cancer, preferably prostate cancer, bladder cancer, kidney
CC cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer,
CC cervical cancer or stomach cancer. The composition can also be used as a
CC vaccine to treat or prevent cancer that expresses or overexpresses
CC 121P1F1. The gene for 121P1F1 is located on chromosome 4q. The present
CC sequence is a 121P1F1 protein (full-length or fragment).
XX
SQ Sequence 190 AA;
Query Match 93.1%; Score 975; DB 8; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.3e-82;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MMEIFSEKDVFOFKDLEKIPKESGTPMSVKEVLQSLVDDGWDVCRIQSTNYNAFP 75
DB 1 MMEIFSEKDVFOFKDLEKIPKESGTPMSVKEVLQSLVDDGWDVCRIQSTNYNAFP 60
QY 76 SKALHARKHKLVELESQISEGSOGRASIOKSIERAKIGRCETERTRLAKELSSLRDRE 135
DB 61 SKALHARKHKLVELESQISEGSOGRASIOKSIERAKIGRCETERTRLAKELSSLRDRE 120
QY 136 QLKAEVEKTKCDPQVVEIRQANKVKAENRPTDNI FALKSNKRGCFEENKIDRTF 195
DB 121 QLKAEVEKTKCDPQVVEIRQANKVKAENRPTDNI FALKSNKRGCFEENKIDRTF 180
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190

Search completed: February 2, 2006, 12:48:42
Job time : 63 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 2, 2006, 12:50:47 ; Search time 43 Seconds

(without alignments)
458.708 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047
Sequence: 1 MSKKKGSLAEKRTTRMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	33.3	210	2 T37610	hypothetical coile
2	197	18.8	128	2 T08972	hypothetical prote
3	168.5	16.1	174	2 S61134	hypothetical prote
4	135.5	12.9	1281	2 JC5368	dynamactin 1 - mouse
5	130.5	12.5	1053	2 A41642	kinectin 1 - chicken
6	121.5	11.6	1356	2 S32763	kinectin 1 - human
7	117	11.2	768	2 T02572	hypothetical prote
8	116.5	11.1	2442	2 T08621	centrosome associa
9	115.5	11.0	880	2 F75103	conserved hypotet
10	114	10.9	284	2 S24972	tropomyosin alpha,
11	114	10.9	764	2 T05409	hypothetical prote
12	113	10.8	199	2 A32183	tropomyosin TPM1 -
13	112	10.7	284	2 JCG199	alpha-tropomyosin
14	112	10.7	285	2 A24199	tropomyosin NM, sk
15	112	10.7	559	2 S49143	EG10 protein - tap
16	112	10.7	1938	2 A45923	skeletal myosin he
17	111	10.6	559	2 A45620	cyclophilin homolog
18	111	10.6	1937	2 T18055	myosin heavy chain
19	110.5	10.6	308	2 T08796	tropomyosin - huma
20	110.5	10.6	629	2 T44607	hypothetical prote
21	110.5	10.6	879	2 C71083	conserved hypotet
22	110	10.5	284	2 I51731	alpha-tropomyosin
23	109.5	10.5	168	2 G86578	CT670 hypothetical
24	109.5	10.5	168	2 B70465	conserved hypotet
25	109.5	10.5	284	2 JCG198	alpha-tropomyosin
26	109.5	10.5	1298	2 E70318	hypothetical prote
27	109.5	10.5	1298	2 T24480	hypothetical prote
28	109.5	10.5	1390	2 S51364	sperm tail-specific
29	109	10.4	284	2 JC2551	tropomyosin alpha

30	109	10.4	284	2 S19691	tropomyosin alpha,
31	109	10.4	676	2 S00084	myosin heavy chain
32	108	10.3	670	2 F84899	hypothetical prote
33	107.5	10.3	1085	2 P66712	hypothetical prote
34	107.5	10.3	1137	2 T19414	hypothetical prote
35	107.5	10.3	1169	2 A54505	p115 homolog - Met
36	107	10.2	280	2 A22165	tropomyosin alpha
37	107	10.2	281	2 A34787	tropomyosin 1 alph
38	107	10.2	284	1 TWRBA	tropomyosin alpha
39	107	10.2	284	2 A39816	tropomyosin 2, fib
40	107	10.2	284	2 B27407	tropomyosin alpha
41	107	10.2	284	2 A25825	tropomyosin alpha
42	107	10.2	284	2 A60597	tropomyosin 2, fib
43	107	10.2	955	2 S24348	myosin heavy chain
44	106.5	10.2	746	2 T47237	myosin II heavy ch
45	106	10.1	1558	2 B71603	RESA-H3 antigen pF

ALIGNMENTS

RESULT 1
T37610
hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Hunt, S.; Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, September 1995
A:Reference number: 221730
A:Accession: T37610
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-210 <HND>
A:Cross-references: UNIPROT:Q09739; UNIPARC:UPI0000139F78; EMBL:Z54096; PIDN:CAA90804.1;
A:Experimental source: strain 972h-; cosmid c13A11
A:Gene: SPDB:SPAC13A11.03
A:Map position: 1
A:Introns: 22/3

Query Match 33.3%, Score 349, DB 2, Length 210;
Best Local Similarity 41.6%, Pred. No. 3.3e-16;
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY	5	KGLSAEKRTTRMEIFSTKDVFOKDEKTAPEKGTAMSVKEVLSIVDGDVDCER	64
DB	4	KGLSLAEKRRRLAEAFHDSKDFQLEVEKLGSK-KQIVLTQVKVLSIVDNDIVKTEK	62
QY	65	IGTSNYVAPPSKALHARKHKLKLEVSQISESQGHASLQKSI--EKAKIGRCETE-EET	121
DB	63	IGTSNYVSPFSDAKRSRESVLSIQADDDDKQSKTLDENISFEKSRKRDGEGENDAN	122
QY	122	FLAKELSLRD-QREQLKAEVEKRYKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA	180
DB	123	QYTLLELHAKSESLGLTKQSLNLRHNCNPFELNGENTKKYMEANLMTDQIHILIAFC	182
QY	181	KRKGFEENKIDRTFGIPEDFD	202
DB	183	RDWGAADTNOIREYCIPEDLD	203

RESULT 2
T08972
hypothetical protein F19B15.200 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08972
R:Bayan, M.; Hilbert, H.; Braum, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16519
A:Accession: T08972
A:Molecule type: DNA

A:Residues: 1-128 <BEV>
A:Cross-references: UNIPROT:Q9S2E5; UNIPARC:UPI00000AAA02; EMBL:AL078470; GSPDB:GN000624
A:Experimental source: cultivar Columbia; BAC clone F19B15
C:Genetics:
A:Gene: ATSP:F19B15.200
A:Map position: 4
A:Introns: 13/3; 52/3; 88/3; 109/3

Query Match
Best Local Similarity 39.8%; Score 197; DB 2; Length 128;
Matches 49; Conservative 23; Mismatches 37; Indels 14; Gaps 3;

Qy 16 MMEIFSTKDVFPQKLEKIAPEKGTAVSVKVLQSLVDGMYDCERTGTSNYWAF 75
Db 1 MLOIFVESQDFFLKELERKMGPK-KGVISQSVKVDVQSLVDVDAKDKIGIS----- 52

Qy 76 SKALHARKHKLVEESQSLSEGSOKHSLQKSIKIAKIGRCETERTRLAKESLRDRE 135
Db 53 ---LRSVQRK---LESDLQSGNKRKLAEVLDOCEALKGRSESEKTEALTLQKDIKKHK 106

Qy 136 QLK 138
Db 107 DLK 109

RESULT 3

S61134
hypochemical protein YGL183c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypochemical protein G1604
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C:Accession: S61134; S64200
R:Betani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Brusch, C.V.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cere
five new genes.
A:Reference number: S61128
A:Accession: S61134
A:Molecule type: DNA
A:Residues: 1-174 <BER>
A:Cross-references: UNIPROT:P53102; UNIPARC:UPI000013B11A; EMBL:X91489; NID:G1143557; PI
R:Brusch, C.V.; Coglievina, M.; Betani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64183
A:Accession: S64200
A:Molecule type: DNA
A:Residues: 1-174 <BRU>
A:Cross-references: UNIPARC:UPI000013B11A; EMBL:Z72705; NID:G1322796; PIDN:CAA96895.1; F
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:MND1
A:Cross-references: SGD:S0003151
A:Map position: 7L

Query Match
Best Local Similarity 27.2%; Score 168.5; DB 2; Length 174;
Matches 46; Conservative 42; Mismatches 68; Indels 13; Gaps 5;

Qy 45 MSUKEVLOSLVD-DQMVDCERTGTSNYWAFPSKALHARKHKLVTLSQSLSEGSOKHSL 103
Db 1 MIVDDLVQOMIDEDVIVEKCGNINITYCFNQTLLQKLYDSSELIKKKIEVKCDIATY 60

Qy 104 OKSIEKA-KIGRCETERTRLAKESLRDREOLKAEVEKYDCDDPOVEIR----- 156
Db 61 KOELDKTLATGRRKFTYQGSYNREALLERKKKIQDIKK-KNSLSQKISIRMDAKI 119

Qy 157 QANK-----VAKAANRWTDNIFAIKSWAKRKGFEENKIDRTFGIPDF 201
Db 120 QENKQRIKLKKVHLKKTNDNIEILIDYLVKKFFLPQIRKRFQIPDF 168

RESULT 4

JCS368

dynactin 1 - mouse
N:Alternate names: p150 Glued
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JCS368
R:Jiang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.
Biochem. Biophys. Res. Commun. 231, 344-347, 1997
A:Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th
A:Reference number: JCS368; MUID:97223454; PMID:9070275
A:Accession: JCS368
A:Molecule type: mRNA
A:Residues: 1-1281 <JAN>
A:Cross-references: UNIPROT:O08788; UNIPARC:UPI0000027AAD; GB:U60312; NID:G2104494; PIDN
A:Experimental source: brain
A:Comment: This protein is a member of the oligomeric dynactin complex that is required
C:Genetics:
A:Gene: Dctn1
A:Map position: 6

Query Match
Best Local Similarity 23.4%; Score 135.5; DB 2; Length 1281;
Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;

Qy 2 SKKGLSAEKRTPMIFSTKDVFPQKLEKIAPEKGTAVSVKVLQSLVDGMYD 61
Db 279 ARKAKALEKRYEMEMADTADAIEMATLDKMAEERASLQOEVBALKEVDLTTD 338

Qy 62 CER1-----GTSNYWAFPSKALHAR-KHKLVEESQSLSEGSOKHSLQKSIK 110
Db 339 LEIKARIEKSGSAASVQLKLESONARLKALVRMDLSSEKQEHYKLOKMEK- 397

Qy 111 KIGRCET-BERTRLAKESLRDREOLKAEVEKYDCDDPOVEIRQANKVAKANR 168
Db 398 KNQLELVQRQERLELOSELQAESESTIDELKEQVDAAGAE-ENVEMLTDNINLEKVE 456

Qy 169 WTDNIPAIKSWAKRKGFEENKIDRTFGIPDF 202
Db 457 LRETVDLEANNENNDYLQENARETELELRQLD 490

RESULT 5

A41642
dynactin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C:Accession: A41642
R:Gill, S.R.; Schroer, T.A.; Sillak, I.; Steyer, E.R.; Sheetz, M.P.; Cleveland, D.W.
J. Cell Biol. 115, 1639-1650, 1991
A:Title: Dynactin, a conserved, ubiquitously expressed component of an activator of ves
A:Reference number: A41642; MUID:92098576; PMID:1836789
A:Accession: A41642
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1053 <GIL>
A:Cross-references: UNIPROT:P35458; UNIPARC:UPI000017C003; GB:X62773; NID:G63920; PID:96
A:Keywords: cytoskeleton

Query Match
Best Local Similarity 12.5%; Score 130.5; DB 2; Length 1053;
Matches 53; Conservative 42; Mismatches 93; Indels 37; Gaps 7;

Qy 2 SKKGLSAEKRTPMIFSTKDVFPQKLEKIAPEKGTAVSVKVLQSLVD 57
Db 101 AKKAKALEKRYEMEMADTADAIEMATLDKMAEERASLQOEVDLSKEVEYLTM 160

Qy 58 GMV---DCERTGTSNYWAFPSKALHARKHKL---VLESQSLSG-SQKASLQKSIK 110
Db 161 LEIKHIEIEKSGSAASVQKLESONARLKALVRMDLSSEKQEHYKLOKMEK 220

Qy 111 KIGRCETERTRLAKESLRDREOLKAEVEKYDCDDPOVEIRQ 157
Db 221 N-----TELSLQQRKLOEEVQAKETVDELKEQVDAALGAENVEITL 267

Qy 158 ANKYAKEANRWTDNIFAISKWAKRKGFEENKIDRTFGIPEDPD 202
Db 268 RNLDEKVRRLRTVGLLEAMENMDELQENARTELELREQD 312

RESULT 6

S32763
kinectin 1 - human
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S32763; I37947
R/Kruppa, G.; Fuetterer, A.; Lemke, H.; Kroenke, M.
submitted to the EMBL Data Library, April 1993
A/Description: Cloning and characterization of TAF, a novel transactivating protein.
A/Reference number: S32763
A/Accession: S32763
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1356 <KRU>
A/Cross-references: UNIPROT:O86UP2; UNIPARC:UPI00000702A8; EMBL:Z22551
R/Futrerer, A.; Kruppa, G.; Kramer, B.; Lemke, H.; Kronke, M.
Mol. Biol. Cell 6, 161-170, 1995
A/Title: Molecular cloning and characterization of human kinectin.
A/Reference number: 137947; MUID:95306853; PMID:7787243
A/Accession: 137947
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1356 <RES>
A/Cross-references: UNIPARC:UPI00000702A8; EMBL:Z22551; NID:G2396163; PIDN:CAA80271.1; PI
C/Genetics:
A/Gene: GDB:KTN1
A/Cross-references: GDB:6165852; OMIM:600653

Query Match 11.6%; Score 121.5; DB 2; Length 1356;
Best Local Similarity 22.7%; Pred. No. 2.2;
Matches 50; Conservative 31; Mismatches 88; Indels 51; Gaps 5;

Qy 3 KKKGLSAEKKRTRMEIFSETKDVLPOLKLEKIAPEKIGITA--MSVKEVLSLVDDGMV 60
Db 1025 RKGNNDLEKRWEMALASTERKQIDPKYNTSKERQOQVAVELAEVLEKLPKPKSV 1084
Qy 61 DCERIGTSNYVAPPSKALH-----ARKKLEVESLSQSGOKIASLOKSIKAKIGRC 115
Db 1085 P-SNLSTGEWHLGFEKKAKEGACGTSGEVAVLEHLKADENHTLLQLECEKYSVLA 1143
Qy 116 ETE-----ERRRLA-KELSLRD 132
Db 1144 ETEGILQKRSVDEENKMKVYKVDSEHKTIKQMSFTSSBOELERLSERKDIENLR 1203
Qy 133 QREOLKAVERKXKDCDPQVVEIRQANKVAKKANRWTDN 172
Db 1204 EREHLEMLEKAEWERSYTVTEVRELKDLTELQKKLDS 1243

RESULT 7

T02572
hypothenical protein At2g39300 [imported] - Arabidopsis thaliana
N/Alternate names: hypothenical protein T16B24.6
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C/Accession: T02572; F84815
R/Rounbley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Croebly, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, August 1998
A/Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A/Reference number: Z14679
A/Accession: T02572
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-768 <Rou>
A/Cross-references: UNIPROT:O80951; UNIPARC:UPI00000A1172; EMBL:AC004697; NID:G3402671;
A/Experimental source: cultivar Columbia
R/Lin, X.; Kaul, S.; Rounbley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vancken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: F84815

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-768 <STO>
A/Cross-references: UNIPARC:UPI00000A1172; GB:AE002093; NID:G3402677; PIDN:AAC28980.1; C
C/Genetics:
A/Gene: T16B24.6; At2g39300
A/Map position: 2
A/Intons: 80/2; 665/3

Query Match 11.2%; Score 117; DB 2; Length 768;
Best Local Similarity 22.1%; Pred. No. 2.4;
Matches 50; Conservative 46; Mismatches 90; Indels 40; Gaps 9;

Qy 1 MSKKGLSAE-----EKTRMEIFSETK-----DVFOL-KOLEKIAPEKIGIT 43
Db 247 MCKEDVVSSELEKRYKEKRVKLLSEBMEKKFLSDCDFISSIVGDIRQWEEBVRGL- 305
Qy 44 AMSYKVLQSLVDGMDCERIGTSNYVAPPSKALHARKHLEV-LESQSGOKIAS 102
Db 306 AFEVLSLRQMDERASTREDIRRVKNDWLLRLKREKTELQVLELDRSSWTS 365
Qy 103 LQSGIEKAKIGRCETERTRLAKELSLRDQEOUKAEVEKYKDCDPQVVEIRQANKVA 162
Db 366 ---KYSEKTV-----EKKRLREKRVLEAHNVSLQRIISFHEKETERIDMIRLDETIV 416
Qy 163 KE-----AANRWTDNIFAISKWAKRKGFEENKIDRTFGIPEDFDYI 204
Db 417 TELSATAEKREBNLFLMQNLSKLQESYT-----GSTDDLQVY 454

RESULT 8

T08621
centrosome associated protein CEP250 - human
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C/Accession: T08621
R/Mack, G.U.; Rees, J.; Sandblom, O.; Balczon, R.; Fritzler, M.J.; Rattner, J.B.
Arthritis Rheum. 41, 551-558, 1998
A/Title: Autoantibodies to a group of centrosomal proteins in human autoimmune sera reac
A/Reference number: Z16462; MUID:98165428; PMID:9506584
A/Accession: T08621
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2442 <MAC>
A/Cross-references: UNIPARC:UPI0000071A1C; EMBL:AF022655; NID:G2832236; PIDN:AAC06349.1;
A/Experimental source: cell line HeLa

Query Match 11.1%; Score 116.5; DB 2; Length 2442;
Best Local Similarity 19.7%; Pred. No. 9;
Matches 46; Conservative 47; Mismatches 64; Indels 77; Gaps 8;

Qy 1 MSKKGLSAEKKRTRMEIFSETKDVLPOLKLE--KIAPEKIGTAMSVKEVLSLVDDG 58
Db 1662 LQKRIQVLEQDQRTQRTKILSE-----DLQIKLSLRREGRLTQROLMQRRABEG 1713
Qy 59 M-----VDCB-----RIGTSNYW 72
Db 1714 KQPSKAKQSGLEHMKLILRDKEKEVCEQGHINHELQELKDLQEQLOGHHRVGT----- 1769
Qy 73 AFPSKALHARKHLEVESLSQSG-----GSGQNASIQSIKAKIGRCETERTRLAKIS 128
Db 1770 ---SLLSQREQEIVLQOQLAEBOGELBEGSLOSQSDAORALAPRDQ-----ELE 1820
Qy 129 SLRQGRDLKAVERKXKDCDPQVVEIRQANKVAKKANRWTDNIFAISKWAKR 182
Db 1821 ALQDQQAQDQEEKVKSKADALQALQAAHTLTKERHGELODH---KEQAKR 1870

submitted to the Protein Sequence Database, April 1996
 A:Reference number: S62997
 A:Accession: S63011
 A:Molecule type: DNA
 A:Residues: 1-199 <POW>
 A:Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:G1301970; PIDN:CAA95953.1; F
 A:Experimental source: strain S288C
 A:Solter-Mira, A.; Salt, J.E.; Ballesta, J.P.G.; Remacha, M.
 submitted to the Protein Sequence Database, April 1996
 A:Reference number: S63018
 A:Accession: S63018
 A:Molecule type: DNA
 A:Residues: 1-199 <SO>
 A:Cross-references: UNIPARC:UPI0000137254; EMBL:Z71355; NID:G1301970; PIDN:CAA95953.1; F
 A:Experimental source: strain S288C
 A:Poehlmann, R.; Philippen, P.
 Yeast 12, 391-402, 1996
 A:Title: Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12
 A:Reference number: S63925; MUID:96267764; PMID:8701611
 A:Accession: S63928
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-199 <POF>
 A:Cross-references: UNIPARC:UPI0000137254; EMBL:X86470; NID:G791101; PIDN:CAA60179.1; PI
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C:Genetics:
 A:Gene: SGD:TPM1
 A:Cross-references: SGD:S0005023; MIPS:YML079c
 A:Map position: 14L
 C:Superfamily: slime mold ribozyme I
 C:Keywords: coiled coil; cytoskeleton

Query Match 10.8%; Score 113; DB 2; Length 199;
 Best Local Similarity 24.7%; Pred. No. 1;
 Matches 46; Conservative 40; Mismatches 54; Indels 46; Gaps 8;
 QY 7 LSAEKRTRMEIFSETKQVDFQKLEKIAPEKIGITAMSVKVLQSLVD-----GMV 60
 Db 13 LEASWQCKYEELKKNKNDLQ-ENVE-----KENGKSLVTYKN-QQLEDEIEKLEAGLS 65
 QY 61 DCEIRIGTSNYWAFPSKALHARKHKL-----EVLSEQLSEG-----SOK 99
 Db 66 DSKQTEQNVKENGQIKSLTYKNHQLSEIEIEKLELSEKQSLSDSHHLSQNNDNFSGK 125
 QY 100 HASLOKSTKAKIGKCEFEERTR-----LAKLSLDRORQLKAEV-----KYDC 147
 Db 126 NQQLSEEDSESDYKLTETKLRRESDLKADQLERRVAALEGRERERKNEELTVKYEDA 185
 QY 148 DPOVE 153
 Db 186 KKEIDE 191

RESULT 13
 JC6199
 alpha-tropomyosin S-1 - axolotl
 C:Species: *Ambystoma mexicanum* (axolotl)
 C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C:Accession: JC6199
 R:Luque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F.
 Gene 185, 175-180, 1997
 A:Title: Differential expression of a novel isoform of alpha-tropomyosin in cardiac and
 A:Reference number: JC6198; MUID:97208870; PMID:9055812
 A:Contents: skeletal muscle
 A:Accession: JC6199
 A:Molecule type: mRNA
 A:Residues: 1-284 <LUD>
 A:Cross-references: UNIPROT:P87349; UNIPARC:UPI00000FBSF3; GB:U33450; NID:G1871357; PIDN
 C:Comment: This protein is a actin-binding protein.
 C:Genetics:
 A:Gene: ATMS-1
 C:Superfamily: tropomyosin
 C:Keywords: actin binding

Query Match 10.7%; Score 112; DB 2; Length 284;
 Best Local Similarity 22.7%; Pred. No. 1.7;
 Matches 48; Conservative 41; Mismatches 74; Indels 48; Gaps 9;
 QY 1 MSKKKGSLAEK-----KRTRMETIFSETKQVDFQ-----LKDEKIAPK-EKGITAMSV 47
 Db 73 LARKKADTAEDSDVASLNRRIQVLVEEELDRAPQRLATQLEKAEKADSEBRGKVTEN 132
 QY 48 KEVQLSLVDGMDVCERIGTSNYWAFPSKALHARKHKLTVLESLSEGSQK---HNSL 103
 Db 133 R-----ALKDEKEMELQEI-----QLEKAKHIAEADRYEAVARKLVITIEDL 176
 QY 104 QKSTIEKXI--GRCTEERTFLAKELSLDRQRLKAEVKYKDCDPQVVEIRQANKV 161
 Db 177 ERAERARLSESGK-----ALEEELKVTNNLSLEQAQKYSQEDKYEIEIKVLTDK 231
 QY 162 AKKANRPTDNIIPAISKWAKKFGFEENKID 192
 Db 232 LKEAETR-----AEFAERTVAKLEKSID 254

RESULT 14
 A24199
 tropomyosin NM, skeletal muscle - human
 C:Species: *Homo sapiens* (man)
 C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 13-Aug-1999
 C:Accession: S06210; A24199
 R:Clayton, L.; Reinach, F.C.; Chumley, G.M.; Macleod, A.R.
 J. Mol. Biol. 201, 507-515, 1988
 A:Title: Organization of the htm(nm) gene. Implications for the evolution of muscle and
 A:Reference number: S02554; MUID:88332987; PMID:3418707
 A:Accession: S06210
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-285 <CLA>
 A:Cross-references: UNIPARC:UPI000013D90D
 R:Reinach, F.C.; Macleod, A.R.
 Nature 322, 648-650, 1986
 A:Title: Tissue-specific expression of the human tropomyosin gene involved in the genera
 A:Reference number: A24199; MUID:86311274; PMID:3018581
 A:Accession: A24199
 A:Molecule type: mRNA
 A:Residues: 1-285 <REI>
 A:Cross-references: UNIPARC:UPI000013D90D; GB:X04201; NID:G37429; PIDN:CAA27798.1; PID:G
 A:Note: an intronless pseudogene resembling this mRNA is also known
 C:Superfamily: tropomyosin
 C:Keywords: alternative splicing; coiled coil; muscle; skeletal muscle

Query Match 10.7%; Score 112; DB 2; Length 285;
 Best Local Similarity 23.5%; Pred. No. 1.7;
 Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;
 QY 1 MSKKKGSLAEK-----KRTRMETIFSETKQVDFQ-----LKDEKIAPK-EKGITAMSV 47
 Db 74 LAEKKAADAEAEVASLNRRIQVLVEEELDRAPQRLATQLEKAEKADSEBRGKVTEN 133
 QY 48 KEVQLSLVDGMDVCERIGTSNYWAFPSKALHARKHKLTVLESLSEGSQKHAALQSI 107
 Db 134 R-----ALKDEKEMELQEI-----QLEKAKHIAEADRYEAVARKLVITIEDL 177
 QY 108 EKAKIGRCETEERTFLA-----KELSLDRQRLKAEVKYKDCDPQVVEIRQANKV 159
 Db 178 ER-----TEBRKELASKSELEELKVTNNLSLEQAQKYSQEDKYEIEIKILT 230
 QY 160 KVAKKANRWTDNIPAIKSWAKKFGFEENKIDRTFGIPED 200
 Db 221 DKLKEAETRAE---FAERSVA-----KLEKTIIDLED 259

RESULT 15
 G49143
 Eg10 protein - tapeworm (*Echinococcus granulosus*)

C:/Species: Echinococcus granulosus
 C:/Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 15-Mar-2004
 C:/Accession: S49143
 R:/Frosch, P.M.; Hartmann, M.; Sygulla, L.; Margutti, P.; Frosch, M.
 submitted to the EMBL Data Library, January 1994
 A:/Description: Identification of a cDNA clone from the larval stage of Echinococcus gran
 A:/Reference number: S49143
 A:/Accession: S49143
 A:/Status: preliminary
 A:/Molecule type: mRNA
 A:/Releases: 1-559 <PRO>
 A:/Cross-references: UNIPARC:UPI0000078113; EMBL:Z29489; NID:G509759; PIDN:CA82625.1; PI
 C:/Superfamily: ezrin/radixin/moesin; protein 4.1 membrane-binding domain homology
 F/12-293/Domain: protein 4.1 membrane-binding domain homology <B41>

Query Match 10.7%; Score 112; DB 2; Length 559;
 Best Local Similarity 27.8%; Pred. No. 3.6;
 Matches 49; Conservative 34; Mismatches 61; Indels 32; Gaps 7;

QY 1 MSKKKGLSAEKRTFMSEIFSETKDVFQKDLKTIAPKEKGTAMSVKELQSLVDDGMV 60
 Db 294 MRRKRSDSIEYQOMKI-----QAKERELKEAERQRLKERLQRMENEQKLELRAQ-MV 347
 QY 61 DCEKIGTSNYWAPSPSKALHAKKHLVLESQLSF-----GSQKGA--SLQKSTEK-AKI 112
 Db 348 EKE-----SDLADMKNKASAYESKIAELMLQOERHARESILQKSDKLAEM 394
 QY 113 GRCEETERTRLAKELSLRDQREQLKAEVEKYKDCDPQVEEIRQANKVAKKAANR 168
 Db 395 NRKLKETRTAASAEERNRMAQRDEVQREVEAK-----VAMAKKEAEKQAQAEAEIR 445

Search completed: February 2, 2006, 12:51:41
 Job time : 45 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 2, 2006, 12:48:52 ; Search time 119 Seconds

(without alignments)
1215.406 Million cell updates/sec

Title: US-10-087-190-3

Perfect score: 1047

Sequence: 1 MSKKKGASAEKRTIMEIF.....FEENKIDRTFGIPEDPYID 205

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047	100.0	205	2	Q9BWT6 HUMAN
2	954	91.1	205	2	Q8K396 MOUSE
3	948	90.5	205	2	Q9D0A1 MOUSE
4	848	81.0	205	2	Q5FV93 XENTR
5	848	81.0	205	2	Q5XGY9 XENTR
6	783	74.8	204	2	Q4SS06 TETNG
7	644	61.5	220	2	Q6DC61 BRARE
8	462	44.1	196	2	Q86E28 SCHJA
9	459	43.8	269	2	Q50VW2 ENTHI
10	440	42.0	230	2	Q8GYD2 ARATH
11	427	40.8	207	2	Q6H432 ORYSA
12	366	35.0	221	2	Q54B86 DICDI
13	362	34.6	161	2	Q5BYT3 SCHJA
14	349	33.3	210	1	MCPT7 SCHPO
15	340.5	32.5	203	2	Q8SUA9 ENCCU
16	340.5	32.5	203	2	Q6WDA3 GIATA
17	340.5	32.5	203	2	Q7QTX0 GIATA
18	332.5	31.8	179	2	Q6Q9F9 ARDAE
19	303	28.9	205	2	Q5SUF7 CRANE
20	277	26.5	196	2	Q7RH53 PLAYO
21	266.5	25.5	211	2	Q6BQUS DEBHA
22	224.5	21.4	299	2	Q5KCA2 CRANE
23	221	21.1	225	2	Q7SCH5 ASHGO
24	213	20.3	427	2	Q4QAN2 LBIMA
25	206.5	19.7	225	2	Q6CSX5 KULIA
26	202.5	19.3	221	2	Q5BCH7 EMENT
27	197	18.8	128	2	Q8SZ85 ARATH
28	191.5	18.3	201	2	Q59RP1 CANAL
29	176.5	16.9	189	2	Q4WPL0 ASPFU
30	175	16.7	222	2	Q6FL56 CANGA
31	168.5	16.1	174	1	YG73_YEAST

32	155.5	14.9	66	2	Q6CSY4 CRYPV	Q6CSY4 cryptospori
33	153.5	14.7	101	2	Q6E679 ANTIO	Q6E679 antonospora
34	136.5	13.0	910	2	Q7T2F8 BRARE	Q7T2F8 brachydantio
35	136	12.9	1395	2	Q4SSB9 TETNG	Q4SSB9 tetradon n
36	135.5	12.9	1281	1	DYNA_MOUSE	008788 mus musculu
37	134.5	12.8	459	2	Q59F36 HUMAN	Q59F36 homo sapien
38	134.5	12.8	890	2	Q6AWB1 HUMAN	Q6AWB1 homo sapien
39	134.5	12.8	890	2	Q6AWB3 HUMAN	Q6AWB3 homo sapien
40	134.5	12.8	1139	2	Q6IQ37 HUMAN	Q6IQ37 homo sapien
41	134.5	12.8	1264	2	Q6NZM3 MOUSE	Q6NZM3 mus musculu
42	134.5	12.8	1278	1	DYNA_HUMAN	Q14203 homo sapien
43	134.5	12.8	1278	2	Q6MZ23 HUMAN	Q6MZ23 homo sapien
44	131.5	12.6	1009	2	Q5RDS4_PONPY	Q5RDS4 pongo pygma
45	131.5	12.6	1280	1	DYNA_RAT	P28023 rattus norv

ALIGNMENTS

```
RESULT 1
Q9BWT6_HUMAN
ID Q9BWT6_HUMAN PRELIMINARY; PRT; 205 AA.
AC Q9BWT6_01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DE GAJ.
GN Name=GAJ;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Solis G., Hofer H.W.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bonak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
EMBL: AY028916; AAH26168.1; -, mRNA.
EMBL: BC032142; AAH32142.1; -, mRNA.
DR Ensembl; ENSG00000121211; Homo sapiens.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 205 AA; 23753 MW; 95B0B14068DA0B51 CRC64;
```

Query Match 100.0%; Score 1047; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 8e-57;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV 60
DB 1 MSKKKGSAEKKRRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV 60

QY 61 DCEIRIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE 120
DB 61 DCEIRIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE 120

QY 121 TRLAKEISLSDQEQKAEVEKTKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180
DB 121 TRLAKEISLSDQEQKAEVEKTKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180

QY 181 KRKGFENKIDRTFGIPEDFDYID 205
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 2

Q8K396 MOUSE

ID Q8K396_MOUSE PRELIMINARY; PRT; 205 AA.

AC Q8K396;

DT 01-OCT-2002 (TRENBLREL. 22, Created)

DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)

DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)

DE GAJ protein.

GN Name=2610034E18R1k;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J;

RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fealy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

RA Buttefield Y.S.N., Kiryushnik M.I., Skalska U., Smallie D.E.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences".

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J;

RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;

RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.

RA EMBL, BC027741, AAH27741.1, -; mRNA.

RA Ensembl, ENSMUSG0000033752; Mus musculus.

RA MGI, MGI:1924165; 2610034E18R1k.

RA InterPro, IPR005647; Mnd1.

RA Pfam, PF03962; Mnd1.1.

RA SEQUENCE 205 AA; 23849 MW; 122C3FA94345120 CRC64;

Query Match 91.1%; Score 954; DB 2; Length 205;
Best Local Similarity 89.8%; Pred. No. 4.1e-51;
Matches 184; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKKRRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV 60
DB 1 MSKKKGSAEKKRRRMMEIFSETKDVPOLKDEKIAPEKGIITMSVKEVQLSLVDDGMV 60

QY 61 DCEIRIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE 120
DB 61 DCEIRIGTSNYWAPPSKALHARKHLEVLSEQLSESGQKHA5LQKSIKAKIGRCETEE 120

QY 121 TRLAKEISLSDQEQKAEVEKTKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180
DB 121 TRLAKEISLSDQEQKAEVEKTKDCDPQVEEIRQANKVAKAANRWTDNIFAIKSWA 180

QY 181 KRKGFENKIDRTFGIPEDFDYID 205
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 3

Q9D0A1 MOUSE

ID Q9D0A1_MOUSE PRELIMINARY; PRT; 205 AA.

AC Q9D0A1;

DT 01-JUN-2001 (TRENBLREL. 17, Created)

DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)

DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)

DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length

DE enriched library, clone:2610034E18 product:GAJ homolog.

GN Name=2610034E18R1k;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=9927253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RT Meth. Enzymol. 303:19-44 (1999).

RN [2]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Atkawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peele G., Quackenbush J.,

RA Schirni L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Blake J.C., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Casavant T.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima U., Mazzaletti J., Mombarra P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Watanabe-Borja A., Yoshida K., Hasegawa Y., Kawai H., Kohzuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RT Nature 409:685-690 (2001).

RN [3]

R1 NUCLEOTIDE SEQUENCE.

RP STRAIN=C57BL/6J; TISSUE=Whole body;

RC The FANTOM Consortium;

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNA.";
RL Nucleic 420:563-573(2002).
[4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunaka T., Teshio H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichannel sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Akakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kuribara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK011664; BAB27765.1; -; mRNA.
DR Ensembl; ENSMUSG0000003752; Mus musculus.
DR MGI; MGI:1924165; 2610034E18Rik.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1
SQ SEQUENCE 205 AA; 23909 MW; 09368E19E424021 CRC64;
Query Match 90.5%; Score 948; DB 2; Length 205;
Best Local Similarity 89.3%; Pred. No. 9,6e-51;
Matches 183; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY 1 MSKKKGLSABERKTRMEIFSETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60
DB 1 MSKKRGLSGEERKTRMEIFPETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60
QY 61 DCEKGTNNYWAFFSKALHARKHLEKLETSQSGSQSHASLOKISAKIGRCEETER 120
DB 61 DCEKGTNNYWAFFSKALHARKHLEKLETSQSGSQSHASLOKISAKIGRCEETER 120
QY 121 TRIAELSLDQREQLAAVEKYKDCPOVEEIRQANKVAKAEANWTNDIPIAKSWA 180
DB 121 AMLAKELSPFDQROQLAAVEKYKRECPQVEEIRRENNKAKAEANWTNDIPIAKSWA 180
QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
DB 181 KRKGFEEESKIDKNGIPEDFDYID 205
RESULT 4
Q5FV93_XENTR PRELIMINARY; PRT; 205 AA.
ID Q5FV93_XENTR PRELIMINARY; PRT; 205 AA.
AC Q5FV93;
DT 10-MAY-2005 (Tremblrel. 30, Created)
GN

DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE MGC97859 Protein.
GN Name=MGC97859;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenoipodinae; Xenopus; Silurana.
OX NCBI_TaxID=83364;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marubini K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.V., Lu X., Gibbs R.A.,
RA Fahney J., Heltan B., Kettleman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhardt D.S.,
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC090139; AAH90139.1; -; mRNA.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1
SQ SEQUENCE 205 AA; 24130 MW; 4F47091BF3BBF00A CRC64;
Query Match 81.0%; Score 848; DB 2; Length 205;
Best Local Similarity 77.1%; Pred. No. 1.3e-44;
Matches 158; Conservative 29; Mismatches 18; Indels 0; Gaps 0;
QY 1 MSKKKGLSABERKTRMEIFSETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60
DB 1 MSKKRGLSGEERKTRMEIFPETKQVFPOLKLEKIAPEKGTITANSVKEVLSVDDGV 60
QY 61 DCEKGTNNYWAFFSKALHARKHLEKLETSQSGSQSHASLOKISAKIGRCEETER 120
DB 61 DCEKGTNNYWAFFSKALHARKHLEKLETSQSGSQSHASLOKISAKIGRCEETER 120
QY 121 TRIAELSLDQREQLAAVEKYKDCPOVEEIRQANKVAKAEANWTNDIPIAKSWA 180
DB 121 SKLAEELSRHRRKELCAEIKYKDCPDVIEIRQSNKAKADVNWNTNDIPIAKSWA 180
QY 181 KRKGFEEENKIDRTFGIPEDFDYID 205
DB 181 KRKGFEEERQIDKNGIPEDFDYID 205
RESULT 5
Q5XGY9_XENLA PRELIMINARY; PRT; 205 AA.
ID Q5XGY9_XENLA PRELIMINARY; PRT; 205 AA.
AC Q5XGY9;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE LOC95113 protein.
GN Name=LOC95113;
GN

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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus; Xenopus.
NCBI_TaxID=8355;
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strassberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Franke C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzyzinski M.I., Skalski U., Smalins D.E.,
RA Schnerch A., Schein J.R., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Klein S., Gerhard D.S.;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084288; AA084288.1; -; mRNA.
DR InceptPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
SQ SEQUENCE 205 AA; 24022 MW; 2EFE64865708262B CRC64;

Query Match 81.0%; Score 848; DB 2; Length 205;
Best Local Similarity 77.6%; Pred. No. 1.3e-44;
Matches 159; Conservative 27; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSKKKGLSAEKRRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGAV 60
DB 1 MSKKRGLSVEEKRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGAV 60
QY 61 DCEKIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQKSHASLOKSIKAKIGRCETEE 120
DB 61 DSEKIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQKSHASLOKSIKAKIGRCETEE 120
QY 121 TRIAKELSLDQKQQLAAVEKYKDCDPQVVEEIRQANKVAKAANRWTNIFAIKSWA 180
DB 121 SKLVEELSLRHRKEELCADLEKCEKCDPVVEEIRQANKVAKADVNRWTNIFAIKSWA 180
QY 181 KRKGFEEKKIDRTGKIPEDFDYID 205
DB 181 KRKGFEEKKIDRTGKIPEDFDYID 205

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DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 18 SCAF1485, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0013672001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
RN
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dastilva C., Salenouat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McGowan P., Bosak S.,
RA Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Searpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Croillat H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA001014485; CA096576.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 204 AA; 23844 MW; CAB21EFF264BA752 CRC64;

Query Match 74.8%; Score 783; DB 2; Length 204;
Best Local Similarity 72.1%; Pred. No. 1.3e-40;
Matches 147; Conservative 28; Mismatches 29; Indels 0; Gaps 0;

QY 2 SKKKGLSAEKRRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGAV 61
DB 1 SKKKGLSVEEKRTMMEIFSETKDVFPOLKDEKIAPEKGTITAMSVKVLQSLVDGAV 60
QY 62 CERIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQKSHASLOKSIKAKIGRCETERT 121
DB 61 CERIGTSNYWAFPSKALHARKHKLKLEVLISQLSGSGQKSHASLOKSIKAKIGRCETERT 120
QY 122 RLAKELSLDQKQQLAAVEKYKDCDPQVVEEIRQANKVAKAANRWTNIFAIKSWA 181
DB 121 SLKLELDLREERRLLAQLEKYKDCPEVVEEKRSNVAKAANRWTNIFAIKSWA 180
QY 182 RKPGFEENKIDRTGKIPEDFDYID 205
DB 181 KKAFADEKINSIKATGIPEDFDYID 204

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RESULT 7
G6DC61_BRARE
ID G6DC61_BRARE PRELIMINARY; PRT; 220 AA.
AC G6DC61_
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Zgc:101017.
GN ORFNames=zgc:101017;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RE NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shemen C.M., Schler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stopleonko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Louquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Roark S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Wuzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Roderiguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Scheraga A., Schein J.E., Jones S.J.W., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Singapore local strain; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC078223; AAH78223.1; -; mRNA.
DR ZFIN: ZDB-GENE-040801-116; zgc:101017.
DR InterPro: IPR005647; Mnd1.
DR Pfam: PF03962; Mnd1; 1.
SQ SEQUENCE 220 AA; 25176 MW; 90DEAA69311F4BF7 CRC64;

Query Match 61.5%; Score 644; DB 2; Length 220;
Best Local Similarity 71.8%; Pred. No. 4,8e-32;
Matches 125; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

QY 1 MSKKKGLAEEKRTMMEIFSETKDVFPOLKLEKIAPEKGIITAMSVKVLQSLVDDGV 60
DB 1 MSKKKGLLEBKRSKMEIFETKOVFOLEKIAPEKGIITAMSVKVLQSLVDDNV 60
QY 61 DCEKIGTSNYWAFPSKALHAKHLEVLSEGLSGSQKHAISLQKSIKAKIGRCETEER 120
DB 61 DTERVGTSNYWAFPSKALHAKHLEVLSEGLSGSQKHAISLQKSIKAKIGRCETEER 120
QY 121 TRIAELSLRQREQLKAEVRYKDCDPQVEEIRQANKVAKKANRTDNI 174
DB 121 EDLAKETALAKQORDQKVEIKYQECDPVAVEIRNINAKVAKKANRTDNI 174

RESULT 8
Q86E28 SCHUA
ID Q86E28 SCHUA PRELIMINARY; PRT; 196 AA.
AC Q86E28;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Clonozepam mRNA sequence.
OS Clonozepam japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxId=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1336;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,

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RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum
RT complementary DNA resource."
RL Nat. Genet. 35:139-147(2003).
DR EMBL: AY223066; AAP06089.1; -; mRNA.
DR InterPro: IPR005647; Mnd1.
DR Pfam: PF03962; Mnd1; 1.
SQ SEQUENCE 196 AA; 23163 MW; B30F6F08BD7123F0 CRC64;

Query Match 44.1%; Score 462; DB 2; Length 196;
Best Local Similarity 47.4%; Pred. No. 6.4e-21;
Matches 92; Conservative 34; Mismatches 68; Indels 0; Gaps 0;

QY 11 EKRTMMEIFSETKDVFPOLKLEKIAPEKGIITAMSVKVLQSLVDDGVDCERIGTSNY 70
DB 2 KSRQMDMPFEKKQDFPOLKLEKIERLCQKEKIGNSVVDVLMVLHVDGLVDTKIGTSY 61
QY 71 YWAFPSKALHAKHLEVLSEGLSGSQKHAISLQKSIKAKIGRCETEERTLAELSL 130
DB 62 FWAFPSKAQKLRNNIEKVTGDIHTRQIQFPTKTSLEBALSKRQTERRNINIELTEL 121
QY 131 RQREQLKAEVRYKDCDPQVEEIRQANKVAKKANRTDNI 190
DB 122 KLESLTAELODLEKHPDRLELRQQLVALDSANRTDNI 181
QY 191 IDRTFGIPEDPDYI 204
DB 182 PCQGFETENPDYI 195

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RESULT 9
Q50VW2 ENTHI
ID Q50VW2 ENTHI PRELIMINARY; PRT; 269 AA.
AC Q50VW2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=182.t00019;
OS Entamoeba histolytica HM-1.IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxId=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1.IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291.
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.U., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Lejpe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagers K., Moule S., Mungall K., Ormond D., Squares R., Whithead S.,
RA Quail M.A., Rabinowitz E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Iohia A.,
RA Foster P.G., Sichertsz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica."
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAFB01000572; EAL45733.1; -; Genomic_DNA.
DR InterPro: IPR005647; Mnd1.
DR Pfam: PF03962; Mnd1; 1.
KW Hypothetical protein.
SQ SEQUENCE 269 AA; 31920 MW; 63AD3885CF0387B3 CRC64;

Query Match 43.8%; Score 459; DB 2; Length 269;
Best Local Similarity 42.9%; Pred. No. 1.4e-20;
Matches 88; Conservative 53; Mismatches 64; Indels 0; Gaps 0;

QY 1 MSKKKGLAEEKRTMMEIFSETKDVFPOLKLEKIAPEKGIITAMSVKVLQSLVDDGV 60

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RA Hauser H., James K., Quiles M., Mohan M.B., Salto T., Buchrieser C.,
 RA Wardrop A., Felder M., Thanagavelu M., Johnson D., Knights A.,
 RA Louesged H., Mungall K., Oliver K., Price C., Quail M.A.,
 RA Urushihara H., Hernandez J., Rabinovitch E., Steffen D., Sanders M.,
 RA Ma J., Kohara Y., Sharp S., Simmons M., Spiegler S., Tivey A.,
 RA Sngano S., White B., Walker D., Woodard J., Winckler T., Tanaka Y.,
 RA Shaubli G., Schleicher M., Weinstein G., Rosenthal A., Cox E.C.,
 RA Chisholm R.L., Gibbs R., Loomis W.F., Platzter M., Kay R.R.,
 RA Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.,
 RT "The genome of the social amoeba *Dictyostelium discoideum*,"
 RL Nature 0:0-0(2005).
 CC -I- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AFRI01000260; EAL61571.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 221 AA; 25864 MW; 21A4FE8BA02A090C CRC64;
 Query March 35.0%; Score 366; DB 2; Length 221;
 Best Local Similarity 34.8%; Pred. No. 5.7e-15;
 Matches 71; Conservative 52; Mismatches 75; Indels 2; Gaps 1
 QY 2 SKKGLSLAEKRTMMEIFSETKDFOLDEKIAPEKGIYAMSVKEVLSLVDDGWD 61
 DB 3 TRRGGMSEEEKKELKEFFHNSNTIYSSKDVSEASKYTGMYQCKETLQWLIDGYN 62
 QY 62 CERIGTSNYVAPSPKALHARKHLEVLSEQLSEGSQXNASLOKSIIEKATIGRCEERT 121
 DB 63 TDKGSSSNFYWSPSPFEEDSKDKITIEQTKLSEFKRIQSTFKKIEQLKSERVSEFT 122
 QY 122 RLAEELSLRQREOLKAVERKYKDCDPQVVEITQANKVKAENRMTDNIFAKSNK 181
 DB 123 KNLKRLQTLKDNKNSFKKELLLY--ADSSLLDDKDRDKIALAANRYTDNISSLRQCD 180
 QY 182 RKFGFEENKIDRTFGIPEDPYID 205
 DB 181 SKVNIRESDFPSTFOIKRPMYLE 204
 RESULT 13
 Q5BYT3 SCHJA
 ID ID O5BYT3 SCHJA PRELIMINARY; PRT; 161 AA.
 AC O5BYT3;
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DS Hypothetical protein.
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeididae;
 OC Schistosomatidae; Schistosomatidae; Schistosoma.
 CC NCBI_TaxID=6182;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Han Z.;
 RL Submitted (MAR-2005) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY811553; AAX27442.1; -, mRNA.
 DR InterPro; IPR000074; APOA1_A4_E.
 DR InterPro; IPR010980; Cyt_c_b562.
 DR InterPro; IPR011029; DEATH_like.
 DR InterPro; IPR005647; Md1.
 DR InterPro; IPR011993; PH_type.
 DR InterPro; IPR008976; PLAT_LH2.
 DR InterPro; IPR011991; Wing_hlx_DNA_bd.
 DR Pfam; PF03962; Md1; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 161 AA; 18748 MW; 9CD91CC2BEC31141 CRC64;
 Query Match 34.6%; Score 362; DB 2; Length 161;
 Best Local Similarity 45.6%; Pred. No. 7.3e-15;
 Matches 73; Conservative 28; Mismatches 59; Indels 0; Gaps 0
 QY 45 MSUYEVLSLVDDGWDCEERTGTSNYVAPSPKALHARKHLEVLSEQLSEGSQXNASLQ 104

Db	1	MSVADYLMISLVHGLDVTDDTIGTSVYFWAPPSSKAAQKRLNNIEKVTDDIHDTNRQIKFRT	60
Qy	105	KSLEBKAKIGCGCEEBRTLRKLEISSLDEQSEOLKAEYKWKDCPPQVEYIRQANKPAC	164
Db	61	RSLSNEALSCKKQDYBERNRLINELTELILLESFLAELODEKHPDRLSELRLQOOLVALD	120
Qy	165	AANRWTDNIFFAISKWAKRKFGEENKIDRTFTGIPDEPDYI	204
Db	121	SANRWTDNIFVIKSWLSNKFSLDEATCRQPELIPENDYI	160
RESULT 14			
MCp7 SCHPO			
ID	MCp7 SCHPO	STANDARD;	PRT; 210 AA.
AC	009739;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	10-MAY-2005 (Rel. 47, Last annotation update)		
DE	Meliotic coiled-coil protein 7.		
GN	Name=mcP7; ORFNames=SPACJ3A11.03;		
OS	Schizosaccharomyces (Fission yeast).		
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;		
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;		
OC	Schizosaccharomycetes.		
OX	NCBI_TaxID=4896;		
RN	[1]		
RP	NCLECTOTIDE SEQUENCE, FUNCTION, AND INTERACTION WITH MEUJ3.		
RX	PubMed=15210864; DOI=10.1093/nar/gkh654;		
RA	Saito T.T., Tougan T., Kasama T., Okuzaki D., Nojima H.;		
RT	"McP7, a meiosis-specific coiled-coil protein of fission yeast,		
RL	associated with MeuJ3 and is required for meiotic recombination."		
	Nucleic Acids Res. 32:3325-3339(2004).		
RN	[2]		
RP	NCLECTOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RX	STRAIN=9712;		
RX	MEDLINE=118548401; PubMed=11859360; DOI=10.1038/nature724;		
RA	Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,		
RA	Brooks J.G., Peat N., Hayles J., Baker S.G., Baeham D., Bowman S.,		
RA	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,		
RA	Gentles S., Goble A., Hamlin N., Harris D.B., Hidalgo J., Hodgson G.,		
RA	Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,		
RA	James K.D., Jones L., Jones M., Leather S., McDonald S., Mclean J.,		
RA	Mooney P., Moulle S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,		
RA	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,		
RA	Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,		
RA	Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,		
RA	Taylor K., Taylor R.G., Tivey A., Welsh S.V., Warren T., Whitehead S.,		
RA	Woodward J.R., Volckaert G., Aert R., Robben J., Grymponrez B.,		
RA	Welchens I., Vannesteels E., Rieger M., Schaefer M., Mueller-Auer S.,		
RA	Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer K., Moestl D.,		
RA	Hilbert H., Borzym K., Langner I., Beck A., Lehnach H., Reinhardt R.,		
RA	Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,		
RA	Goffeau A., Cadieu E., Dreano S., Gloux S., Leclaire V., Mottier S.,		
RA	Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,		
RA	Lucas M., Roche M., Galliard C., Tallada V.A., Garzon A., Rhode G.,		
RA	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,		
RA	Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,		
RA	Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,		
RA	Shpakovetski G.V., Usery D., Barrell B.G., Nure P.;		
RT	The genome sequence of Schizosaccharomyces pombe."		
RL	Nature 415:871-880(2002).		
CC	-I- FUNCTION: Required for meiotic recombination.		
CC	-I- SUBUNIT: Interacts with meuJ3.		
CC	-----		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	EMBL: AB189985; BAD24247.1; -; Genomic_DNA.		
CC	EMBL: Z54096; CAJ90804.1; -; Genomic_DNA.		

DR "PIR, T37610, T37610.
DR GenedB_Spombe; SPAC13A11.03; -.
DR GO; GO:0000785; C:chromatin; IDA.
DR GO; GO:0007131; P:meiotic recombination; IGI.
DR GO; GO:0007129; P:synapsis; IMP.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
KM Coiled coil; Complete proteome; Melosis.
FT COILED 77 148 Potential.
SQ SEQUENCE 210 AA; 24224 MW; FA546F070A37665 CRC64;

Query Match 33.3%; Score 349; DB 1; Length 210;
Best Local Similarity 41.6%; Pred. No. 6e-14;
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLAEEKRTMMEIFSETKDVOLKLEKIAPEKGITAMSVKVLQSLVDGMVDCER 64
DB 4 KGLSLAEKRRRLLEAIFHDSKDFOLKEVEKLGSK-KQIVLOTVDLQSLVDNDIVKTEK 62
QY 65 IGTSNYYWAPPSKALHARKHLEVLSEQLSEGSQKHASLQKSI--EKATIGRCETE-ERT 121
DB 63 IGTSNYYWSPSPDAKRSRESVLSLQALQDLDLKQKSKTLDENISPEKSKRDNEGTEENDAN 122
QY 122 RLAKELSLRD-QREQLKAEVEKYKDCDPQVEVERIQANKYAKAEANRWTNIFAISKMA 180
DB 123 QYTELHLAKSEELKLTQLSNLRNCPETELKNENTKRYMEANMLMTDQIHLLAFC 182
QY 181 KRKFGFEENKIDRTFGIPEDFD 202
DB 183 -RDMGADTNQIREYCSTPEDLD 203

RESULT 15
Q8SUA9 ENCCU
ID Q8SUA9_ENCCU PRELIMINARY; PRT; 203 AA.
AC Q8SUA9_01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein ECU10.1600.
GN OrderedLocustNames=ECU10.1600;
OS Encephalitozoon cuniculi.
OC Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_Taxid=6035;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Kacinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensler G., Barde V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590449; CAD25881.1; -; Genomic_DNA.
DR InterPro; IPR005647; Mnd1.
DR Pfam; PF03962; Mnd1; 1.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 203 AA; 23743 MW; DFE33A65A1A28A42 CRC64;

Query Match 32.5%; Score 340.5; DB 2; Length 203;
Best Local Similarity 35.1%; Pred. No. 1.9e-13;
Matches 71; Conservative 50; Mismatches 72; Indels 9; Gaps 3;

QY 7 LSAEERTMMEIFSETKDVOLKLEKIAPEKGITAMSVKVLQSLVDGMVDCERIG 66
DB 6 MKSDQKSLLEITIGSKSFFDLQELTESLGSK-KGIIVNTIKRIIQQLVDDGLVTAERKG 64
QY 67 TSNYYWAPPSKALHARKHLEVLSEQLSEGSQKHASLQKSI-EKATIGRCETEERTRLAKE 126
DB 65 TSNLYWSPASRGIQKKDKURCKELMEECERMSQDICRKEIYINENKMSKHYTBERNELNK 124

QY 127 LSSL-----RQREQLKAEVEKYKDCDPQVEVERIQANKYAKAEANRWTNIFAISKMAKR 182
DB 125 LNALMKIEQDQRB---ELGKFERTDPIAYDKLVAORKENADECNRIIDNVFIIDYICS 180
QY 183 KFGFEENKIDRTFGIPEDFDYI 204
DB 181 KFGMEKSEFNSFGIIPDDYI 202

Search completed: February 2, 2006, 12:51:01
Job time : 122 secs

TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
US-09-799-250B-5

Query Match 33.3%; Score 349; DB 2; Length 200;
Best Local Similarity 41.6%; Pred. No. 3.2e-26;
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLSAEKRRTMMEIFSETKDVOLFQKDEKIAPEKKGITAMSVKEVLSQSLVDGWDGND 64
DB 1 KGLSLAEKRRRLLEAIFHDSKDFQJKEVEKLGSK-KQIVLOTVDVLSQSLVDNDIVKTEK 59
QY 65 IGTNNYWPSPSKALHARKHKLKLEVLSEQSLSGSQKASLOKSI--EKAKIGRCETE-BRT 121
DB 60 IGTNNYWPSPSKALHARKHKLKLEVLSEQSLSGSQKASLOKSI--EKAKIGRCETE-BRT 119
QY 122 RLAEKLSLRD-QREQLKAEVEKTKCDPQVEEIRQANKYAKAEANWTNIFAIKSWA 180
DB 120 QYTFELHAKESSEKLTQTLQSLNHNCHNPETFEKLNMENTKXKMEANLMTDQIHLLAFC 179
QY 181 KRKGFEEKTKIDRTFGIPEDPD 202
DB 180 -RDMGADTNQIREYCSIPEDLD 200

RESULT 6
US-09-799-250B-721

Sequence 721, Application US/09799250B
Patent No. 6924358
GENERAL INFORMATION:
APPLICANT: Rene S. Hubert
APPLICANT: Pia M. Chailica-Bid
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Faris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovics
TITLE OF INVENTION: 121PIPI: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.340S01 (51582003400)
CURRENT FILING DATE: 2003-07-14
CURRENT APPLICATION NUMBER: US/09/799,250B
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 721
LENGTH: 200
TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
US-09-799-250B-721

Query Match 33.3%; Score 349; DB 2; Length 200;
Best Local Similarity 41.6%; Pred. No. 3.2e-26;
Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps 5;

QY 5 KGLSAEKRRTMMEIFSETKDVOLFQKDEKIAPEKKGITAMSVKEVLSQSLVDGWDGND 64
DB 1 KGLSLAEKRRRLLEAIFHDSKDFQJKEVEKLGSK-KQIVLOTVDVLSQSLVDNDIVKTEK 59
QY 65 IGTNNYWPSPSKALHARKHKLKLEVLSEQSLSGSQKASLOKSI--EKAKIGRCETE-BRT 121
DB 60 IGTNNYWPSPSKALHARKHKLKLEVLSEQSLSGSQKASLOKSI--EKAKIGRCETE-BRT 119
QY 122 RLAEKLSLRD-QREQLKAEVEKTKCDPQVEEIRQANKYAKAEANWTNIFAIKSWA 180
DB 120 QYTFELHAKESSEKLTQTLQSLNHNCHNPETFEKLNMENTKXKMEANLMTDQIHLLAFC 179
QY 181 KRKGFEEKTKIDRTFGIPEDPD 202
DB 180 -RDMGADTNQIREYCSIPEDLD 200

RESULT 7
US-09-248-796A-14485

Sequence 14485, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14485
LENGTH: 260
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-14485

Query Match 18.3%; Score 191.5; DB 2; Length 260;
Best Local Similarity 27.1%; Pred. No. 1.1e-10;
Matches 59; Conservative 47; Mismatches 75; Indels 37; Gaps 8;

QY 1 MSKKKGLSAEKRRTMMEIFSETKDVOLFQKDEKIAPEKKGITAMSVKEVLSQSLVDGWDGND 60
DB 60 MPKKGGLQGEKRLSALNWFQSDHMFYTLKEIKESKSKQCKIPQMKELVLALVEGLV 119
QY 61 DCEIGTNNYWPSPSKALHARKHKLKLEVLSEQSLSGSQKASLOKSIKAK-----IGR 114
DB 120 EQRGCGTTLNLYWSP-----YLOHKKQ-----QETHRLNNTIANLTERDSLICR 165
QY 115 C-FTEERTLAKELSLR-----DREQLKAEVEKTKCDPQVEEIRQANKYAKAEANA 166
DB 166 CKDEGVNQTHERASKTRFCDQSLERIDISQSLQSLKDSBS--VE-----NLVTSIAF 218
QY 167 NRWTNIFAIKSWAKRKGFEEKTKIDRTFGIPEDPDYI 204
DB 219 --FSDSIDDIDICVLSRQGLMTTLKTEFELPLEEERI 254

RESULT 8
US-09-538-092-1321

Sequence 1321, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Gloc, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurateSeqFormatter Version 0.9
SEQ ID NO 1321
LENGTH: 1270
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321

Query Match 12.8%; Score 134.5; DB 2; Length 1270;
Best Local Similarity 23.4%; Pred. No. 0.00032;
Matches 50; Conservative 43; Mismatches 106; Indels 15; Gaps 5;

QY 2 SKKKGLSAEKRRTMMEIFSETKDVOLFQKDEKIAPEKKGITAMSVKEVLSQSLVDGWDGND 61

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4
D0      271 ARKEKALBEAKERMEEMADTADALIMATLIDKEMAEESIQOEVEALKEVDELTTD 330
QY      62 CER1-----GTSNYMAFPSPKALTAR-KHKLEVPESQUSSEGSOKHASLOKSIERA 110
D0      331 LEILKAETBEKSDGDAASSYOLKQLEBQNALKDALVRRKIDSSSSKOEHVLOKIMEK- 389
QY      111 KIGRCET--EERTRLAKETSLDRQEQKAEVEKYKCDPQVVEEIRQANKVAKAEANR 168
D0      390 KNOELEVRQOQERIQOEELISOABSTIDELKEQVDALGAE-EVEMVLTDRNLNLEKRE 448
QY      169 WTDNIFAIKSWAKRKFGEENKIDRTFGJIPEDF 202
D0      449 LRETVGDLEAMNEMNDELQENARETLEIRBOLD 482

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RESULT 9
 US-09-104-324B-4
 Sequence 4, Application US/09104324B
 Patent No. 6232460
 GENERAL INFORMATION:
 APPLICANT: T rec1,
 TITLE OF INVENTION: Ozlem; Sabin, Ugur; pfrendschub, Michael
 TITLE OF INVENTION: Methods For Diagnosis and Treating Cancers,
 TITLE OF INVENTION: And Methods For Identifying Pathogenic Markers In A Sample Of
 TITLE OF INVENTION: No. 6232460mal Cells

```

1  NUMBER OF SEQUENCES: 4
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Fulbright & Jaworski LLP
4  STREET: 666 Fifth Avenue
5  CITY: New York City
6  STATE: New York
7  ZIP: 10103
8
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
11
12 COMPUTER: IBM
13 OPERATING SYSTEM: PC-DOS
14 SOFTWARE: Wordperfect
15
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/104,324B
18 FILING DATE: 25-June-1998
19
20 CLASSIFICATION: 435
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/892,702
24 FILING DATE: 15-July-1997
25
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Hanson, No. 6232460man D.
28 REGISTRATION NUMBER: 30,946
29 REFERENCE/DOCKET NUMBER: LUD 5491
30
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (212) 318-3000
33 TELEFAX: (212) 752-5958
34
35 INFORMATION FOR SEQ ID NO: 4:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 976 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40
41 US-09-104-324B-4

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Query Match	11.2%;	Score 117;	DB 2;	Length 976;
Best Local Similarity	23.9%;	Pred. No. 0.012;		
Matches	63;	Conservative	38;	Mismatches 85;
			Indels	78;
			Gaps	13;

[illegible][illegible]

```

RESULT 10
US-09-538-092-1339
Sequence 1339, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Glot, Iolc
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/179,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormatter Version 0.9
SEQ ID NO 1339
LENGTH: 976
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number Q15431
US-09-538-092-1339

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Query Match	11.2%;	Score 117;	DB 2;	Length 976;
Best Local Similarity	23.9%;	Pred. No. 0.012;		
Matches	63;	Conservative	38;	Mismatches 85;
				Indels 78;
				Gaps 13

```

QY      3 KKKGISAE--KRTAMEI--PSETQV-----FQJDLKIAKPKKGIYAMSYKVEL 51
Db      413 QKSSSELEEMTKLTNNKKEVELEELKVVIGKETTLLYENKQFEXIAEELG--TEQELIGLL 471
QY      52 QSL---VDDGWDCEIGTSGTNYAFAFSKAL-----HARKHLEYLE-- 90
Db      472 QAREKVDHLEIQLAIITTSQGYYSKEVYDLTELBNELKNTLTELTSHCNKJLSNKEPL 511
QY      91 -----SQLSBGSQKXASLQKSIIRKAKIGRETEEBRTLAEBSLROQRQ 136
Db      532 QETSDMTLELNQOEDINNKKQEBRMQLQIT--NLQETETQIRNELYVREELKORDE 589
QY      137 LKAEVETKD--CD-----PQVEVEIRQANKVAKK--AANRWTDNIFAIR----- 177
Db      590 VKCTLDKBSBNCNNLRQVYENKNTIIEIQSNKALKKKGTASKQJLNYEIKVNTLELE 649
QY      178 -SMARKRG-----PEENKI 191
Db      650 LESAKQKQGEITDYQKEIEDKKI 673

```

```

RESULT 11
US-09-914-259-55
; Sequence 55, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914.259

```

;; CURRENT FILING DATE: 2000-11-21
;; NUMBER OF SEQ ID NOS: 180
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 55
;; LENGTH: 284
;; TYPE: PRT
;; ORGANISM: Sus scrofa
US-09-914-259-55

Query Match 10.9%; Score 114; DB 2; Length 284;
Best Local Similarity 23.2%; Pred. No. 0.0043;
Matches 52; Conservative 37; Mismatches 61; Indels 74; Gaps 11;

QY 1 MSKKKGLSAE---EKRTTMEIFSETKDVFOQLKLEKIAPEKKGITAMSVKVEVLSLVDD 57
DB 73 LAEKATDAEADVASINRRIQLVEEELDRQAQ-----ERLA-----TALQKLEAKADE 122
QY 58 ---GMVDCERIGTSNYWAPPSKALHAR---KHKLEVLSEQLSEGSQK----- 100
DB 123 SERGM-----KYIESRAQKDEKMEIOETQLKEA---KHTAEDADRKYE 163
QY 101 -----ASLOKTEKAKI---GRCTEERTRLAKESLRDQREOLKAEVKYKCD 148
DB 164 EVARKLVIESDLEPAERAEISBGKC-----ALIEBELKTVTNLKSLEAQAEKYSQKE 218
QY 149 PQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKID 192
DB 219 DKYEEIKVLSDKLKEAETR-----AEFAERSVTLKESID 254

RESULT 12
US-09-914-259-62
;; Sequence 62, Application US/09914259
;; Patent No. 6495336
;; GENERAL INFORMATION:
;; APPLICANT: Makowski, Lee
;; APPLICANT: Hyman, Paul
;; APPLICANT: Williams, Mark
;; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
;; FILE REFERENCE: 8471-010-999
;; CURRENT APPLICATION NUMBER: US/09/914,259
;; CURRENT FILING DATE: 2000-11-21
;; NUMBER OF SEQ ID NOS: 180
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 62
;; LENGTH: 284
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
US-09-914-259-62

Query Match 10.8%; Score 113.5; DB 2; Length 284;
Best Local Similarity 21.1%; Pred. No. 0.0048;
Matches 48; Conservative 48; Mismatches 78; Indels 53; Gaps 8;

QY 2 SKKKGLSA-EKRTTMEIFSETKDVFOQLKLEKIAPEKKGITAMSVK-EVLQSLVDDGM 59
DB 45 AKETLIRASEBERDRLVEELHKAEDSLAAD-ETPAKAEADVASINRRIQLVEEELDRQAQ 103
QY 60 VDCERIGTSNYWAPPSKALHARKHKLVELESQSEGSQK----- 99
DB 104 ---ERLATATLQKLEBAEKAADESERGMKVISSRAQKDEKMEIOETQLKEAKHIAEDADR 160
QY 100 -----HASLOKTEKAKI---GRCTEERTRLAKESLRDQREOLKAEVKYK 145
DB 161 KYEEVARKLVIESDLEPAERAEISBGKC-----ALIEBELKTVTNLKSLEAQAEKYS 215
QY 146 DCDPQVVEIRQANKVAKAANRWTDNIFAIKSWAKRKFGFEENKID 192
DB 216 QKEKYEIEIKVLSDKLKEAETR-----AEFAERSVTLKESID 254

RESULT 13
US-09-248-796A-20275

;; Sequence 20275, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstein et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 20275
;; LENGTH: 630
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-20275

Query Match 10.7%; Score 112.5; DB 2; Length 630;
Best Local Similarity 23.8%; Pred. No. 0.018;
Matches 49; Conservative 43; Mismatches 79; Indels 35; Gaps 8;

QY 3 KKKGLSAEKKRTTMEIFSETKDVFOQLKLEKIAPEKKGIT-AMSVKVEVLSLVDDGMV 60
DB 158 KTKNSDTELKLEKQLELEKVK-----LDLTADEKLGITERIALKSELETVNNSG-- 210
QY 61 DCEIGTSNYWAPPS---KALHARKHKLVEVL-----ESQLSEGSQKHAISLOSI----- 107
DB 211 ---LSTTSELAAULTKTVKSLSEKEKEELOFISGNKSKLELDYIQHSDISEKLTDEL 266
QY 108 -EKAKIGRCEERTRLAKESLRDQREOLKAEVKYKCDPQVVEIRQANKVAKAEA 166
DB 267 KEKTKQPDSSKGLTELENDLTSTKKELETETKTQSKRNLBERDKXIVLKNLEBELLK 326
QY 167 NRWTDNIFAIKSWAKRKFGFEENKID 192
DB 327 N---DN-----SGAKKLELEKYSKLE 344

RESULT 14
US-09-914-259-43
;; Sequence 43, Application US/09914259
;; Patent No. 6495336
;; GENERAL INFORMATION:
;; APPLICANT: Makowski, Lee
;; APPLICANT: Hyman, Paul
;; APPLICANT: Williams, Mark
;; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
;; FILE REFERENCE: 8471-010-999
;; CURRENT APPLICATION NUMBER: US/09/914,259
;; CURRENT FILING DATE: 2000-11-21
;; NUMBER OF SEQ ID NOS: 180
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 43
;; LENGTH: 284
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-914-259-43

Query Match 10.7%; Score 112; DB 2; Length 284;
Best Local Similarity 23.5%; Pred. No. 0.0068;
Matches 52; Conservative 41; Mismatches 72; Indels 56; Gaps 9;

QY 1 MSKKKGLSAEKK---RTTMEIFSETKDVFO-----LKDEKIAPK-EKGITAMSV 47
DB 73 LAEKKAADAABAVASINRRIQLVEEELDRQAQERLATATLQKLEBAEKAADESERGMKVIEN 132
QY 48 KEVLSLVDDGMVDCERIGTSNYWAPPSKALHARKHKLVELESQSEGSQKHAISLOSI 107
DB 133 R---ALKDEKMEIOET-----QKKAHIAEDADRKYEEVARKLVIIIBDL 176

Oy*	108	KKAKIGRCETERETKLA-----	KEISLROFROQLAEVYKDCDPVVEEIRQAN	159
Db	177	ER-----TERRAELAEKCELBELNANVTNNLKS	LAQNAEKYSQKDKYEEETKILT	229
Oy	160	KVAKEAANRWTDNIPAKISMNAKGRKPFEE	NKIKIDRTGCIQIED	200
Db	230	DKLKEAETRAE---PAERSVA-----	KEKTIIDDLDD	258

```

RESULT 15
US-09-538-092-918
: Sequence 918, Application US/09538092
: Patent No. 675314
: GENERAL INFORMATION:
: APPLICANT: Glot, Loic
: APPLICANT: Mansfield, Traci A.
: TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
: FILE REFERENCE: 15966-542
: CURRENT APPLICATION NUMBER: US/09/538,092
: CURRENT FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: 60/127,352
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: 60/178,965
: PRIOR FILING DATE: 2000-02-01
: NUMBER OF SEQ. ID NOS: 1387
: SOFTWARE: CurataseqFormatter Version 0.9
: SEQ ID NO 918
: LENGTH: 1937
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (0)..(0)
: OTHER INFORMATION: Polypeptide Accession Number P13535
: US-09-538-092-918

```

Query Match	10.6%	Score 111	DB 2	Length 1937
Best Local Similarity	23.1%	Pred. No. 0.11		
Matches 54, Conservative	42	Mismatches 88	Indels 50	Gaps 9

```

QY      4 KKGJSAEKRIRAMEIIFSEETDVFQOLKLEKAPK-----EKGIRAMS-----V 47
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
Db      1361 QRALSKANSBVAQMRKTETDAIQCTEELBEKKKLALQDGEABEHVANAANKASLEKT 1420
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
QY      48 KEVLOSLVDGMDVDCERIGTS-----NYMAFPKALHARKKLEVLSESQISEGQ 98
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
Db      1421 KQRIQNEVEEDLMDLYERSNAACALDKQRNF-----DKVLSBWKQKTEBFOALBESAQ 1475
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
QY      99 KHASIQSIEAK-----IGRCET--EERTPLAKELSLSDQ-----RQQLKAE 140
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
Db      1476 ESRSLSTELFKVKVNYEESLDQLETLRENNKULOEOEIDLTQOIAEGKOIHELEKIKQ 1535
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
QY      141 VEKKKDQPVVEEIRQANKYAKA--ARWTDNIIAITSMAKRGKGFENKIDR 193
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||
Db      1536 VEQEK-CETQALAEASLEHSEKILIRIQETELQVSEVDKRTAKEDDEIDQ 1568
      :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: ||

```

Search completed: February 2, 2006, 12:52:34
Job time : 48 secs

GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-3

Query Match 100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLOKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLOKSIKAKIGRCETEE 120
QY 121 TRIAKELSLRDQEQKAEVEKYKDCDPQVEEIRQANKVAKAANRMTDNIFAISWA 180
DB 121 TRIAKELSLRDQEQKAEVEKYKDCDPQVEEIRQANKVAKAANRMTDNIFAISWA 180
QY 181 KRKGFENKIDRTFGIPEDFDYID 205
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 3
US-10-087-190-14
; Sequence 14, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-14

Query Match 100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLOKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLOKSIKAKIGRCETEE 120
QY 121 TRIAKELSLRDQEQKAEVEKYKDCDPQVEEIRQANKVAKAANRMTDNIFAISWA 180
DB 121 TRIAKELSLRDQEQKAEVEKYKDCDPQVEEIRQANKVAKAANRMTDNIFAISWA 180
QY 181 KRKGFENKIDRTFGIPEDFDYID 205
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 4
US-10-087-190-20
; Sequence 20, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Mangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-20

Query Match 100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKGSAEKKRRMEIFSETKDVOLKLEKIAPEKIGITAMSVKVLQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLOKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSKALHARKHKLTVLSQSLSEGSQKASLOKSIKAKIGRCETEE 120
QY 121 TRIAKELSLRDQEQKAEVEKYKDCDPQVEEIRQANKVAKAANRMTDNIFAISWA 180
DB 121 TRIAKELSLRDQEQKAEVEKYKDCDPQVEEIRQANKVAKAANRMTDNIFAISWA 180
QY 181 KRKGFENKIDRTFGIPEDFDYID 205
DB 181 KRKGFENKIDRTFGIPEDFDYID 205

RESULT 5
US-10-087-190-21
; Sequence 21, Application US/10087190

```
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-21

Query Match
Best Local Similarity 100.0%; Score 1047; DB 4; Length 205;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
QY 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
DB 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
QY 181 KRKGFPEENKIDRTFGIPEDFYID 205
DB 181 KRKGFPEENKIDRTFGIPEDFYID 205

RESULT 6
US-10-087-190-22
Sequence 22, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-22
```

```
Query Match
Best Local Similarity 100.0%; Score 1047; DB 4; Length 205;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
QY 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
DB 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
QY 181 KRKGFPEENKIDRTFGIPEDFYID 205
DB 181 KRKGFPEENKIDRTFGIPEDFYID 205

RESULT 7
US-10-087-190-61
Sequence 61, Application US/10087190
Publication No. US2003022397A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 61
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-61

Query Match
Best Local Similarity 100.0%; Score 1047; DB 4; Length 205;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
DB 1 MSKKKGSAEKRTRMEIFSETDVFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
DB 61 DCEIGTSNYWAPPSPKALHARKKLEVLSEQLSEGSQKASLQKSIKAKIGRCETEE 120
QY 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
DB 121 TRLAKELSLDQREQLKAEVEKYKDCDPQVEEIRQANKVAKAANWTNIFAISMA 180
QY 181 KRKGFPEENKIDRTFGIPEDFYID 205
DB 181 KRKGFPEENKIDRTFGIPEDFYID 205

RESULT 8
US-10-408-765A-1821
```

```
; Sequence 1821, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Baby, Boin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Marnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1821
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1821
```

```
Query Match 100.0%; Score 1047; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
   1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
Db 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60

Qy 61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120
   61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120
Db 61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120

Qy 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180
   121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180
Db 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180

Qy 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
   181 KRKGFEEKNKIDRTFGIPEDFDYID 205
Db 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
```

```
RESULT 9
US-11-125-805-2
; Sequence 2, Application US/11125805
; Publication No. US20050208059A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Mary Faris
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovitz
; TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.34US01 (511582003400)
; CURRENT APPLICATION NUMBER: US/11/125,805
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/09/799,250B
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-125-805-2
```

```
Query Match 100.0%; Score 1047; DB 6; Length 205;
Best Local Similarity 100.0%; Pred. No. 4e-78;
```

```
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
   1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
Db 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60

Qy 61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120
   61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120
Db 61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120

Qy 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180
   121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180
Db 121 TRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSWA 180

Qy 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
   181 KRKGFEEKNKIDRTFGIPEDFDYID 205
Db 181 KRKGFEEKNKIDRTFGIPEDFDYID 205
```

```
RESULT 10
US-10-087-190-44
; Sequence 44, Application US/10087190
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: Agenys, Inc.
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Mangmeo
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1 USERFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-44
```

```
Query Match 99.0%; Score 1036.5; DB 4; Length 206;
Best Local Similarity 99.5%; Pred. No. 3e-77;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
   1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60
Db 1 MSKKKGSAEKKRTMMEIFSETKQVDFQKDLKIAPEKGITAMSVKVLQSLVDDGMV 60

Qy 61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 119
   61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 119
Db 61 DCEIRIGTSNYWMAFPSPKALHARKHKLTVLSQSLSEGSQKHA5LOKSIKAKIGRCETEE 120

Qy 120 RTRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSW 179
   120 RTRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSW 179
Db 120 RTRLAKEISSLRDQREQLKAEVEKYKDCDPQVVEIRQANKVAKAANRWTDNIPAIKSW 180

Qy 180 AKRKGFEENKIDRTFGIPEDFDYID 205
   180 AKRKGFEENKIDRTFGIPEDFDYID 205
Db 180 AKRKGFEENKIDRTFGIPEDFDYID 206
```

```
RESULT 11
US-10-087-190-45
; Sequence 45, Application US/10087190
; Publication No. US2003022397A1
; GENERAL INFORMATION:
```

```
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
FILE REFERENCE: 51158-20034.20
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45
LENGTH: 206
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-45
```

Query Match 99.0%; Score 1036.5; DB 4; Length 206;
Best Local Similarity 99.5%; Pred. No. 3e-77;
Matches 205; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 MSKKKGSAEKKRTMMEIFSETKDVFPQKLEKAPKEKGTMTMSVYVQSLVDDGMV 60
DB 1 MSKKKGSAEKKRTMMEIFSETKDVFPQKLEKAPKEKGTMTMSVYVQSLVDDGMV 60
QY 61 DCEIGTSNYWAPPSKALHARKHKLAEVLESQ-LSEGSQKASLQKSIIEKAKIGRCETEE 119
DB 61 DCEIGTSNYWAPPSKALHARKHKLAEVLESQ-LSEGSQKASLQKSIIEKAKIGRCETEE 120
QY 120 RTRLAKELSLRDQREQLAEVYKDCDPQVVEIRQANKVAKAANRWTDNI PAIKSW 179
DB 121 RTRLAKELSLRDQREQLAEVYKDCDPQVVEIRQANKVAKAANRWTDNI PAIKSW 180
QY 180 AKRKFGEENKIDRTFGIPEDPDYID 205
DB 181 AKRKFGEENKIDRTFGIPEDPDYID 206
```

RESULT 12
US-10-087-190-24

; Sequence 24, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:

```
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
FILE REFERENCE: 51158-20034.20
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 198
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-24
```

Query Match 96.6%; Score 1011; DB 4; Length 198;

Best Local Similarity 100.0%; Pred. No. 3.5e-75;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 5 KGLSAEKKRTMMEIFSETKDVFPQKLEKAPKEKGTMTMSVYVQSLVDDGMVDCER 64
DB 1 KGLSAEKKRTMMEIFSETKDVFPQKLEKAPKEKGTMTMSVYVQSLVDDGMVDCER 60
QY 65 IGTSNYWAPPSKALHARKHKLAEVLESQ-LSEGSQKASLQKSIIEKAKIGRCETERTLA 124
DB 61 IGTSNYWAPPSKALHARKHKLAEVLESQ-LSEGSQKASLQKSIIEKAKIGRCETERTLA 120
QY 125 KELSRLDQREQLAEVYKDCDPQVVEIRQANKVAKAANRWTDNI PAIKSWAKRF 184
DB 121 KELSRLDQREQLAEVYKDCDPQVVEIRQANKVAKAANRWTDNI PAIKSWAKRF 180
QY 185 GFEEKNIDRTFGIPEDPD 202
DB 181 GFEEKNIDRTFGIPEDPD 198
```

RESULT 13
US-11-125-805-720

; Sequence 720, Application US/11125805
; Publication No. US20050208059A1
; GENERAL INFORMATION:

```
APPLICANT: Pia M. Challita-Bid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1: A TISSUE SPECIFIC PROTEIN
FILE REFERENCE: 129.34US01 (511582003400)
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US/11/125,805
NUMBER OF SEQ ID NOS: 721
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 720
LENGTH: 198
TYPE: PRT
ORGANISM: Schizosaccharomyces pombe
US-11-125-805-720
```

Query Match 96.6%; Score 1011; DB 6; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.5e-75;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 5 KGLSAEKKRTMMEIFSETKDVFPQKLEKAPKEKGTMTMSVYVQSLVDDGMVDCER 64
DB 1 KGLSAEKKRTMMEIFSETKDVFPQKLEKAPKEKGTMTMSVYVQSLVDDGMVDCER 60
QY 65 IGTSNYWAPPSKALHARKHKLAEVLESQ-LSEGSQKASLQKSIIEKAKIGRCETERTLA 124
DB 61 IGTSNYWAPPSKALHARKHKLAEVLESQ-LSEGSQKASLQKSIIEKAKIGRCETERTLA 120
QY 125 KELSRLDQREQLAEVYKDCDPQVVEIRQANKVAKAANRWTDNI PAIKSWAKRF 184
DB 121 KELSRLDQREQLAEVYKDCDPQVVEIRQANKVAKAANRWTDNI PAIKSWAKRF 180
QY 185 GFEEKNIDRTFGIPEDPD 202
DB 181 GFEEKNIDRTFGIPEDPD 198
```

RESULT 14

US-10-087-190-13
; Sequence 13, Application US/10087190
; Publication No. US20030223997A1
; GENERAL INFORMATION:

*APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Mangao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-13

Query Match 93.1%; Score 975; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 3e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 MMEIFSEKDVFOQLKDLKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 75
DB 1 MMEIFSEKDVFOQLKDLKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 60
QY 76 SKALHARKHKLVELESQSLSGSQKASLQKSIIEKAKIGRCETERTRLAKELSLRDRE 135
DB 61 SKALHARKHKLVELESQSLSGSQKASLQKSIIEKAKIGRCETERTRLAKELSLRDRE 120
QY 136 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIPAIKSWAKKFGFEENKIDRTF 195
DB 121 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIPAIKSWAKKFGFEENKIDRTF 180
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190

RESULT 15
US-10-087-190-19
; Sequence 19, Application US/10087190
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Afar, Daniel E. H.
; APPLICANT: Ge, Mangao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; FILE REFERENCE: 51158-20034.20
; CURRENT FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-19

Query Match 93.1%; Score 975; DB 4; Length 190;

Best Local Similarity 100.0%; Pred. No. 3e-72;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 MMEIFSEKDVFOQLKDLKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 75
DB 1 MMEIFSEKDVFOQLKDLKIAPEKGIITAMSVKEVLQSLVDGAVDCERIGTSNYNAFP 60
QY 76 SKALHARKHKLVELESQSLSGSQKASLQKSIIEKAKIGRCETERTRLAKELSLRDRE 135
DB 61 SKALHARKHKLVELESQSLSGSQKASLQKSIIEKAKIGRCETERTRLAKELSLRDRE 120
QY 136 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIPAIKSWAKKFGFEENKIDRTF 195
DB 121 QLKAEVEKYKDCDPQVVEEIRQANKVAKAANRWTDNIPAIKSWAKKFGFEENKIDRTF 180
QY 196 GIPEDFDYID 205
DB 181 GIPEDFDYID 190

Search completed: February 2, 2006, 12:56:14
Job time : 173 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 2, 2006, 12:53:27 ; Search time 8 Seconds

(without alignments)
300.275 Million cell updates/sec

Title: US-10-087-190-3

Sequence: 1 MSKKGLSAEKRTRMEIF.....FEENKIDRTFGIPEDFYID 205

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Published Applications_AA New:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEM_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	11.2	976	US-11-155-288-20	Sequence 20, App1
2	108.5	10.4	860	US-11-019-711-59	Sequence 59, App1
3	106	10.1	1786	US-11-196-400-3	Sequence 3, App1
4	100.5	9.6	1976	US-11-069-834-52	Sequence 52, App1
5	100.5	9.6	2665	US-11-124-368A-214	Sequence 214, App
6	98	9.4	2668	US-11-124-368A-215	Sequence 215, App
7	97.5	9.3	1976	US-11-069-834-54	Sequence 54, App
8	96	9.2	171	US-10-821-234-994	Sequence 994, App
9	95.5	9.1	1960	US-11-069-834-48	Sequence 48, App
10	94	9.0	284	US-10-821-234-1532	Sequence 1632, App
11	93	8.9	248	US-10-878-556A-175	Sequence 175, App
12	91.5	8.7	1992	US-11-069-834-58	Sequence 58, App1
13	91.5	8.7	2000	US-11-069-834-56	Sequence 56, App1
14	91.5	8.7	664	US-10-878-556A-44	Sequence 44, App1
15	91	8.7	1995	US-11-069-834-60	Sequence 60, App1
16	91	8.7	2261	US-10-995-561-600	Sequence 600, App
17	91	8.7	2261	US-10-511-545-1	Sequence 1, App1
18	91	8.7	2261	US-11-055-309A-9	Sequence 9, App1
19	91	8.7	2261	US-11-055-309A-10	Sequence 10, App1
20	90.5	8.6	2101	US-10-857-780-23	Sequence 23, App1
21	90.5	8.6	2101	US-10-857-780-23	Sequence 23, App1
22	90	8.6	776	US-10-821-234-1171	Sequence 1171, App
23	89.5	8.5	1388	US-10-821-234-1143	Sequence 1143, App
24	89.5	8.5	1410	US-10-878-556A-136	Sequence 136, App
25	89.5	8.5	1586	US-10-821-234-901	Sequence 901, App

26	88.5	8.5	1404	US-10-878-556A-169	Sequence 169, App
27	88	8.4	1299	US-10-821-234-1145	Sequence 1145, App
28	88	8.4	3803	US-10-995-561-773	Sequence 773, App
29	88	8.4	3960	US-10-995-561-771	Sequence 771, App
30	88	8.4	5335	US-10-995-561-777	Sequence 777, App
31	88	8.4	5406	US-10-995-561-774	Sequence 774, App
32	88	8.4	5415	US-10-995-561-779	Sequence 779, App
33	88	8.4	5464	US-10-995-561-775	Sequence 775, App
34	87.5	8.4	1732	US-10-055-877-147	Sequence 147, App
35	86	8.2	1663	US-10-055-877-148	Sequence 148, App
36	85	8.1	227	US-11-215-658-12	Sequence 12, App1
37	85	8.1	693	US-10-873-528-185	Sequence 185, App
38	84.5	8.1	448	US-10-793-626-1728	Sequence 1728, App
39	84.5	8.1	1641	US-10-877-346-40	Sequence 40, App1
40	84.5	8.1	2107	US-10-995-561-827	Sequence 827, App1
41	84.5	8.1	2480	US-10-995-561-825	Sequence 825, App
42	84.5	8.1	3116	US-10-995-561-826	Sequence 826, App
43	84	8.0	663	US-11-196-475-70	Sequence 70, App1
44	84	8.0	663	US-11-196-475-78	Sequence 78, App1
45	84	8.0	1652	US-10-995-561-663	Sequence 663, App

ALIGNMENTS

RESULT 1
US-11-155-288-20
; Sequence 20, Application US/1155288
; Publication NO. US20060008468A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNA 050A
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 976
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-155-288-20

Query Match 11.2% Score 117; DB 7; Length 976;
Best Local Similarity 23.9%; Pred. No. 0.094;
Matches 63; Conservative 38; Mismatches 85; Indels 78; Gaps 13;

3 KKKGLSABE--KRTTMEI-PSFTQV-----FOLKDEKIPKKEGIRAMSVKEVL 51
413 QKKSLEBEMTKLTNNKEVELEELKVGEEKTLTYNNKQFKIABELG-TEOBILGL 471
52 OSL---VDDGWDCRIGTSNYTAPPSKAL-----HARKKLEVL-- 90
472 QAREKVEHDLRLQLTAITTSBOYYSKEYKDLTELENEKTLKTELSHONKSLNKEVLT 531
91 -----SOLSEGSQKHAISLOKSIKAKIGRCETEERTLAKELSLDQREQ 136
532 QETSDMTLEKNQGDINNKKQKBERMLKQIE--NLQETETQLRNELEVREBKQKRB 589
137 LKAIEKTKD-CD-----PQVEERQANKYAKK--ANRRTDNIFAK----- 177
590 VKCKDKSEBENCNNLRKOVENKRYIBELQENKALKKKGLAESKOLNVEIKVKNLELE 649
QY 178 -SWAKKFG-----FEENKI 191
DB 650 LSAKQKFGELITDTYQKLEIDKTI 673

RESULT 2

```
US-11-019-711-59
; Sequence 59, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchenev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Paturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Verneet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigara, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eichen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; PRIOR FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Myosin Tail
; OTHER INFORMATION: Consensus Sequence
US-11-019-711-59

Query Match      10.4%; Score 108.5; DB 7; Length 860;
Best Local Similarity 28.1%; Pred. No. 0.36;
Matches 43; Conservative 27; Mismatches 58; Indels 25; Gaps 6;

QY      13 RTRMMEISFTDVQLDLKIAKPKGKITMSYKVEYQSLVYDGMVDCERIGTSNYW 72
DB      126 RKKQDAINEISE--QISQLQKQAK-----AEKESQLQAEVDLLAQLDISI----- 171
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QY      73 AFPSKA-LHARKKLEVLSEQLSEGSQKHSLSQKSIKAKIGRCETERTRIAKELSLR 131
DB      172 ---TKAKINAEK-KAKQLSEQLSEIQLVLDLQRLQDL-----TSQKSLQSENSDLT 221

QY      132 DQESQLAEVEKYDCDQPVVEEIRQANKVAK 164
DB      222 RQLEAEAEQVNSLSKLSQSLSEAKRSISE 254

RESULT 3
US-11-196-400-3
; Sequence 3, Application US/11196400
; Publication No. US20050287166A1
; GENERAL INFORMATION:
; APPLICANT: DRUTHE, PIERRE
; APPLICANT: DAUBERSIES, PIERRE
; TITLE OF INVENTION: MALALIAL PRE-BRYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773USDIV
; CURRENT APPLICATION NUMBER: US/11/196,400
; PRIOR FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: US/09/742,096
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,462
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: P. falciparum
US-11-196-400-3

Query Match      10.1%; Score 106; DB 7; Length 1786;
Best Local Similarity 18.7%; Pred. No. 1.3;
Matches 47; Conservative 55; Mismatches 77; Indels 72; Gaps 9;

QY      2 SKKKGLSAEKRRTMMEIFSETKD-----VFQDLKRIAPKEKGTMTMSYKVIQ 52
DB      1186 SKERTESIKDKKQVSLVEEVQNDMDSEKVIELKMEBELMKD-----AVEINDITS 1241

QY      53 SLVDD---GMVDCERIGTSNYWAFPSKALHARKKLEVLSEQLSEGSQ-----KHSLS 103
DB      1242 KLIBETQELNEVADLI-----KOMERKLEKALSBDSEKIIDAKDPTL 1286

QY      104 QKSIKKA-----KIGRCETERTRIAKELSLRQDQKAEVEKYKDCDQPVVEI 155
DB      1287 EKVIEEHHDTTTLDEVELDKVEDKLEK-VSDLKDLBIDLKVEKEIKELSESLBDY 1345

QY      156 RQANKV-----AKEAARWNTNIPAIKSMARKFGFSEKTKIDR 193
DB      1346 KELKTITETDILSEKKEIKEDHFKFEEBAEISIKDLBIDLKVESSLVE-----EKKKLE 1401

QY      194 TFGIPEDFYI 204
DB      1402 VHELKEVEYHI 1412

RESULT 4
US-11-069-834-52
; Sequence 52, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
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; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 1976
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-069-834-52

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Query Match          9.6%; Score 100.5; DB 7; Length 1976;
Best Local Similarity 24.7%; Pred. No. 4;
Matches 49; Conservative 40; Mismatches 50; Indels 59; Gaps 9;

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QY 10 EKRTRMEIFSETGV-FOLKLEKIAPKKSG-----ITMS-----VKFVL--- 51
DB 934 EBRNQLIQ--NEKKMOAHIODLSEQDLDEEGANQKIQLEKVIYAEAKIKKMEEVLLLE 991
QY 52 -----QSLVDDGAVDCERIGTSNYWAFPSKALHARK--HKLLEYLSQLSGSKH 100
DB 992 DQNSKFIKKEKLMERIAEC-----SSQLAEERKAKOLAKIRNKQVWISDLBERLKE 1046
QY 101 ASLQKSTKAKIGRCETERRRLAKELSLRDQEQQLAEVEKYQCDPQVEEIR--- 156
DB 1047 EKTQLEKAK-----RLLDEETDLOQIAELQAVDELKYQTLKKEEELQCALA 1097
QY 157 -----QANKYAKE 164
DB 1098 RGDETHLHKNNAKLVARE 1115

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RESULT 5
US-11-124-368A-214
; Sequence 214, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CLO01524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 2665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-214

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Query Match          9.6%; Score 100.5; DB 7; Length 2665;
Best Local Similarity 20.3%; Pred. No. 5.7;
Matches 41; Conservative 49; Mismatches 71; Indels 41; Gaps 7;

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QY 1 MSKKGLSAEER--TRMEIFSETGVFOLKLEKIAPKKGIYAMSVKVELQSLVDP-- 56
DB 1737 IDKLRGIVSEKTEINISNOQKLEHSDALKAQDLK--IOEELRIAHMHLKE--QOETIDKL 1793
QY 57 -----DGMVDCER-IGTSNYWAFPSKALHARKKLEVLSEQLSGSKHSLQSKI 107
DB 1794 RGIVSEKTDKLSNMQKDLJENNAKIQEKIQELKANEHQLITLKQVNETQKVSMEQLK 1853
QY 108 EKAK-----IGRCETE-----EETRLAKELSLRDQEQQLAEVE 142
DB 1854 KQIKDQSLTSLKLEINENLAQKLEHLENLEMKSVKERDNLRRVEETLKLERDQLKESLQ 1913

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QY 143 KYKCDPQVEEIRQANKYAKE 164
DB 1914 ETKARDLEIQOELKTARMLSK 1935

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RESULT 6
US-11-124-368A-215
; Sequence 215, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CLO01524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 215
; LENGTH: 2668
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-368A-215

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Query Match          9.4%; Score 98; DB 7; Length 2668;
Best Local Similarity 20.7%; Pred. No. 8.8;
Matches 42; Conservative 47; Mismatches 72; Indels 42; Gaps 7;

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QY 1 MSKKGLSAEER--TRMEIFSETGVFOLKLEKIAPKKGIYAMSVKVELQSLVDP-- 57
DB 1740 IDKLRGIVSEKTEINISNOQKLEHSDALKAQDLK--IOEELRIAHMHLKE--QOETIDKL 1796
QY 58 -GMDVCERIGTSNYWAFPS-----KALHARKKLEVLSEQLSGSKHSLQSKS 106
DB 1797 RGIVSEKTDKLSNMQKDLJENNAKIQEKIQELKANEHQLITLKQVNETQKVSMEQLK 1856
QY 107 IEKAK-----IGRCETE-----EETRLAKELSLRDQEQQLAEV 141
DB 1857 KQIKDQSLTSLKLEINENLAQKLEHLENLEMKSVKERDNLRRVEETLKLERDQLKESL 1916
QY 142 EKYKCDPQVEEIRQANKYAKE 164
DB 1917 QETKARDLEIQOELKTARMLSK 1935

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RESULT 7
US-11-069-834-54
; Sequence 54, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; PRIOR FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 54
; LENGTH: 1976
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-11-069-834-54

Query Match
Best Local Similarity 23.6%; Pred. No. 6.8;
Matches 41; Conservative 37; Mismatches 61; Indels 35; Gaps 7;

Qy 1 MSKKGLSAEKRTRMEIFSETKDVFLQKLE-KIAPEKGTITMSYKVELQSLVDDGM 59
Db 878 MERGHQQLLEKKNILAEQLQAEITLFAAEEMRARAIAKKQ-----ELEETIHDLSEKVE 932

Qy 60 VDCERIGTSNYMAFPSPKALHARKHKLIV-----LESQI--SGSGOKHASLQKSTIEKATIG 113
Db 933 EEBER-----NQLONEKKKQWQAHITQDLEESQDSEBGAQKQLQLEKVTAEAKIK 981

Qy 114 RCTEERTRLAKELSLDQR-----EQLKAEVEKYKCDPQVEEIRQANVAK 163
Db 982 KME-----EETLLEDQNSKPIKEXKKLMEDRIAESQSLAEERAKNVLAK 1027

RESULT 8
US-10-821-234-994
; Sequence 994, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 994
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-994

Query Match
Best Local Similarity 20.7%; Pred. No. 0.49;
Matches 36; Conservative 38; Mismatches 48; Indels 52; Gaps 6;

Qy 19 IFSETKDVFLQKLEKIA-----PKKGTITMSYKVELQSL 54
Db 20 LFTWASSDIQVLEKRAAGAFELILSPRSKESVPEPPLSPKKKQDLSLEIQKLEAA 79

Qy 55 VDDGVNDERIGTSNYMAFPSPKALHARKHKLIVLESQLSEGSQHASLQKSTIEKATIGR 114
Db 80 EE-----RRKSHAEVLVKQIAEKREKEVEYLQKAIENNNFS 116

Qy 115 CETERTRIAKELSLDQR--QLKAEVEKYKCDPQVEEIRQANVAKAAN 167
Db 117 KMAEE--KLTHKMEANKENREQMAAKLEIRLEKQKH-IEEVRK-NKESKQPAD 166

RESULT 9
US-11-069-834-48
; Sequence 48, Application US/11069834
; Publication No. US20050276811A1
; GENERAL INFORMATION:
; APPLICANT: CARROLL, MICHAEL C.
; APPLICANT: MOORE JR., FRANCIS D.
; APPLICANT: HECHTMAN, HERBERT B.
; TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF
; FILE REFERENCE: CRA-002.01
; CURRENT APPLICATION NUMBER: US/11/069,834
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: 60/588,648
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; PRIOR FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: 60/549,123
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 48
; LENGTH: 1960
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-069-834-48

Query Match
Best Local Similarity 24.1%; Pred. No. 9.6;
Matches 51; Conservative 37; Mismatches 65; Indels 59; Gaps 9;

Qy 8 SAEKRTRMEIFSETKDVFLQKLEKIAPEKGTITAM-----SVKEVLQSLVDDGMVDC 62
Db 1382 TAEAKRQLQ-----KOLEGLSQLEKRVAAVYDLKTKETRLQQLDLDLVLDL 1429

Qy 63 --ERIGTSNYMAFPSPKALHARKHKLIVL-----ESQISEGSQKIAS 102
Db 1430 DHQKQSVN-----LEKKQKFFQDLAEKTTISAKVAERDRAREKREKTKALS 1480

Qy 103 LQKSI-----KAKIGCETERTRIAKELSLDQRQLKAEVEKYKCDPQVEEIR- 156
Db 1481 LARLEAMEQKALERLNKQPTKM--EDLWSSKDVGKSVHELEKSRALAEQVEEMKT 1539

Qy 157 -----QANKVAKAANRWTDNITFAIKSWAKR 182
Db 1540 QLELEDELQATDEAKRLVENVLQAKMAQFHR 1571
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RESULT 10
US-10-821-234-1632
; Sequence 1632, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1632
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1632

Query Match
Best Local Similarity 24.5%; Pred. No. 1.3;
Matches 51; Conservative 30; Mismatches 73; Indels 54; Gaps 8;

Qy 2 SKKGLSAEKRTRMEIFSETKDVFLQKLEKIAPEKGTITMSYKVELQSLVDD----G 58
Db 67 AQEKLEQAEKATTAEDVAVSLNRIQLVEBELDRAOERLATAQLKEBAKADESERG 126

Qy 59 MVDCERIGTSNYMAFPSPKALHAR-----KHKLEVLSQLSEGSQKH----- 100
Db 127 M-----KVIENDAMKDEEMLEIOEMQLKA--KHIABEDRKYEVAR 167

Qy 101 -----ASLQKSTIEKAKIGCETERTR-IAKELSLDQRQLKAEVEKYKCDPQVE 153
Db 168 KLIVLEGLSESRARV-----ASPRANQLDEELRTMQALKSLSAEEESTKEDKYE 223

Qy 154 EIRQANKVAKAANRWTDNITFAIKSWAK 181
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